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Catch-age models for Pacific herring: Evaluation of alternative assumptions about fishery and stock dynamics and alternative error distributions

Modèle des prises selon l'âge pour le hareng du Pacifique : évaluation d'autres hypothèses à propos de la pêche et de la dynamique des stocks et d'autres distributions de l'erreur

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ABSTRACT

The herring stock assessment catch-age model (EASM) was designed for Pacific herring and includes assumptions unique to those stocks. A new catch-age model (NASM) was recently developed for a B.C. herring objective based fisheries management evaluation. The two models differ in some of their assumptions about the fisheries and population dynamics, and it is not clear which should be used in the annual stock assessment process.

We present another catch-age model, HCAM, which incorporates the structure and assumptions of both the EASM and the NASM, with the purpose of determining which assumptions of the EASM and NASM models result in better performance. To the extent possible, objective criteria are used to assess model performance.

Both the EASM and NASM models over-weight the data (that is, residuals tended to be over-dispersed relative to the error assumed for individual data components) and both models have strong age-related patterns in the residuals from fitting the age composition data. The EASM analyses have strong retrospective bias in abundance estimates; for the NASM-like analyses the retrospective patterns are not as large and relatively unbiased.

We evaluated numerous implementations of the HCAM, attempting to minimize the areas of concern with the EASM and the NASM implementations. An implementation of this model was developed that we believe has better performance than either the EASM or the NASM, although it incorporates aspects of both those models. Diagnostics from the HCAM implementation that we believe indicate better performance are; a reduction in the magnitude of the retrospective pattern; a reduction in the magnitude of the age-related pattern in age-composition residuals, and better coherence between the assumed and empirical estimates of the lack of model fit to the data.

RÉSUMÉ

Le modèle existant de la structure d'âge (MSAE) utilisé pour l'évaluation des stocks de hareng a été conçu précisément pour le hareng du Pacifique et comporte des hypothèses qui sont propres à ces stocks. Un nouveau modèle de la structure d'âge (NMSA) a récemment été bâti en vue de réaliser une évaluation de la gestion par objectif de la pêche du hareng de la C.-B. Les deux modèles diffèrent quant aux hypothèses posées à propos de la pêche et de la dynamique des populations et l'on ne sait pas encore lequel devrait être utilisé pour le processus annuel d'évaluation des stocks.

Nous présentons un autre modèle des prises selon l'âge (MPAH) auquel ont été intégrées la structure et les hypothèses des précédents, soit le MSAE et le NMSA, en vue de déterminer quelles hypothèses du MSAE et du NMSA donnent la meilleure performance. Dans la mesure du possible, des critères objectifs sont utilisés pour évaluer la performance du modèle.

Les deux modèles, le MSAE et le NMSA, entraînent une surpondération des données (c.-à-d. que les valeurs résiduelles tendent à être trop dispersées par rapport à l'erreur hypothétique des différents éléments de données) et ils affichent de fortes tendances selon l'âge dans les données résiduelles découlant de l'application des données de la composition par âge. Les analyses selon le MSAE montrent un fort biais rétrospectif dans l'estimation de l'abondance. Dans les analyses selon le NMSA, les tendances rétrospectives ne sont pas aussi fortes et sont relativement non biaisées.

Nous avons évalué de nombreuses applications du MPAH, en essayant de minimiser les points de préoccupation du MSAE et du NMSA. Nous avons développé une application de ce modèle qui, à notre avis, donne une meilleure performance que le MSAE ou le NMSA, bien qu'elle comporte des aspects de ces deux modèles. Les résultats de l'application du MPAH qui nous permettent de dire qu'il a une meilleure performance sont les suivants : une réduction de l'ampleur de la tendance rétrospective, une diminution de l'ordre de grandeur de la tendance liée à l'âge dans les valeurs résiduelles de la composition selon l'âge et une meilleure cohérence entre les estimations hypothétiques et empiriques du manque d'ajustement du modèle aux données.

INTRODUCTION

B.C. herring stock assessments have been based on statistical catch-age model analyses since the early 1980's (Haist and Stocker 1984). The catch-age model used in the assessments was specifically designed for the Pacific herring stocks and thus has assumptions and resulting parameterizations that are unique to those stocks. The model has been revised over the years, but the basic structure and assumptions remain the same (eg. Schweigert 2005a, Schweigert 2005b). This model, which recently was given the name EASM (existing age-structured model), uses maximum likelihood estimation.

Recently, an alternative age-structured model was developed and used to reconstruct the B.C. herring stocks. The purpose of the new models was to function as an operating model for an objective-based fishing management evaluation of B.C. herring stocks (Fu et al. 2004). This new model, called NASM (new age-structured model), adopts some structural assumptions that differ from the EASM and the model allows investigation of alternative assumptions about herring dynamics. A major difference between the EASM and the NASM is the estimation of annual natural mortality rates. Additionally, NASM incorporates stock-recruitment functions and estimates deviations from average selectivity functions. The NASM is based on Bayesian estimation, which allows a consistent method to estimate uncertainty of both the estimated and derived parameters (Punt and Hilborn 1997). Simulation-estimation experiments suggest that in certain circumstances NASM provides more consistent parameter estimates (Fu et al. 2004).

Catch-age analyses provide the basis for setting annual herring TACs, so it is imperative that the best possible analytical methods be used. It is likely that there are aspects of both the EASM and the NASM that will result in superior model performance. To the extent possible, comparison of model performance should be based on objective criteria.

The purpose of the work presented in this paper is to develop a generic model (ie. the computer code) for analyses of the herring fisheries data, and to determine which assumptions of the EASM and NASM models result in better performance. Objective criteria are used to assess improvements in performance. The new model, HCAM for herring catch-age model, can replicate the dynamics modelled by EASM and NASM, and allows for some additional assumptions to be investigated.

The first part of this paper provides a general description of the HCAM model. Then results from an EASM-like and a NASM-like implementation of the model are presented. Finally, alternative model assumptions are evaluated to find those that result in consistent analyses of the B.C. herring fisheries data. Some additional structural options in the HCAM model (eg multi-region and two sex analyses) are not investigated here.

DESCRIPTION OF THE GENERALIZED HERRING CATCH-AGE MODEL

In this section we provide an overview of the generalized herring catch-age model (HCAM), including descriptions of the options for population and fishery dynamics and the likelihoods used in fitting to observations. A detailed model description is provided in Appendix A. Differences between the EASM and the NASM implementations are also described here.

MODEL DYNAMICS

The state, or current status of the populations, partitions the fish by characters that define their distinct status. The possible characters include: age class, sex, maturity (called availability to reflect their being available to fisheries), and stock. Changes in state, or transition processes include: recruitment, natural mortality, fishing mortality, and ageing.

Time steps or fishing periods

The HCAM structure allows for a variable number of time steps (periods) each year, where each time step may have an associated fishery and natural mortality. The EASM analyses separate the annual herring catch into three categories: a winter fishery; a spawning-season seine fishery (SN); and a spawning-season gillnet fishery (GN). For the NASM analyses, data from the first two of these fisheries (winter and SN) are combined and only two fisheries are modelled.

Selectivity/Availability Options

The model structure allows the distinction of fish that are available to the fishery from those that are not. The separation into available and non-available fish, which is modelled as age-specific, occurs at the beginning of the year. The available fish are subject to both fishing and natural mortality while the non-available fish are subject to natural morality. The availability parameterization is used in EASM but not in NASM.

A number of options are coded for the parameterization of age-specific fishery selectivity and age-specific availability. These include: fixed at 1; age-based logistic functions; a size-based logistic function; and free-at-age (see Appendix A for descriptions of these).

Deviations from the prescribed availability-at-age or selectivity-at-age can be estimated. For availability deviations this adds an additional parameter for each year and for selectivity deviations this adds an additional parameter for each fishery. The methods for including deviations are different for the alternative parameterizations of availability and selectivity and are described in the Appendix A.

EASM uses a weight-based logistic function to parameterize GN selectivity and fixes selectivity at 1 for the other fisheries. The EASM analyses also estimate deviations from the age-specific availability. NASM uses an age-based logistic function (with fixed parameters) for both the GN and the SN (combined winter and spawning-season) fisheries, and estimates deviations.

Fishery Dynamics and the Catch Equations

The fishery dynamics can be modelled using either the instantaneous (Baronov) form of catch equations where fishing and natural mortality are simultaneous or a discrete form of catch equations where natural mortality occurs prior to fishing. Solution of the catch equations can be done analytically (using an iterative Newton-Raphson algorithm for the instantaneous form) or by estimating parameters that define fully-selected fishing mortality rates. In the first case the

implied assumption is that there is no error in the catch data while the second case acknowledges error in the catch data.

The EASM analyses are based on the instantaneous fishing mortality equations and estimate model parameters that define the fully-selected fishing mortality rates. NASM uses the discrete form of the catch equations and these are solved analytically. The NASM analyses have both fisheries occurring simultaneously at the end of the year (ie. after natural mortality).

Natural Mortality

A number of options representing different assumptions about natural mortality rates are available. These include: fixed or estimated values for the constant natural mortality rate; age-dependent natural mortality rates; annual deviations from an average natural mortality rate; and a time-series approach using a "random walk" (Gudmundsson 1994) to parameterize annual changes in natural mortality rates. These are described in Appendix A.

EASM estimates a single natural mortality rate. NASM estimates annual deviations in natural mortality and uses a recursive approach (Appendix A) so that the average natural mortality is not an estimated "free" parameter.

Stock-Recruitment Assumptions

A Beverton-Holt type stock-recruitment relationship is coded in HCAM, using the "steepness" parameterization (Mace and Doonan 1988, Francis 1992). Estimated parameters of the stock-recruitment relationship are: R_0, the average recruitment at the unfished equilibrium biomass level (B_0); steepness (h), the fraction of R_0 that is expected at 20% of B_0; and the variance of the residuals from the stock-recruitment relationship (σ_r).

EASM does not assume a stock-recruitment relationship. The NASM herring analyses assume a Beverton-Holt stock-recruitment relationship and also estimate autocorrelation in the recruitment residuals. We did not code the option for estimating autocorrelation in the recruitment residuals because experience suggests that it is not possible to simultaneously estimate the autocorrelation and variance parameter (σ_r).

Initializing the Populations

The populations can be initialized either by estimating parameters for the number of fish in each age-class in the first year of the analysis, or by assuming equilibrium conditions in the first year. Equilibrium conditions can be estimated for populations that are subject only to natural mortality prior to the first year or they can be estimated for populations that are subject to a constant exploitation rate and natural mortality prior to the first year.

HCAM models a "plus" age-class, which accumulates all fish of the "plus" age and older.

EASM initializes the populations by estimating the number of fish in each age-class in the first year (1951). NASM initializes the populations by assuming equilibrium conditions (with no harvest) in 1943, and assumes there is no catch taken until 1951. EASM has a "plus" group at age 7 and NASM has a plus group at age 10.

Ageing Errors

Two options for estimating ageing errors are incorporated into HCAM. The first option estimates two vectors for ageing errors – these represent the probabilities at each age of under-ageing fish by one year and the probabilities at each age of over-ageing fish by one year. The second option is based on an ageing error model developed by Francis (2003). The basis of this model is the assumption that for each ring in the ageing structure there is a probability that the ring will not be counted and second probability that two rings will be counted. Thus, the probability of ageing error increases with age and may be asymmetrical.

The EASM and the NASM model do not estimate ageing errors.

PARAMETER ESTIMATION

HCAM is structured for Bayesian estimation, though by not specifying parameter priors maximum likelihood estimation can be done. HCAM uses the ADMB model package (Otter Research 2000). ADMB allows multi-phase estimation, where initially some parameters are held fixed while the minimization is carried out, then some of the fixed parameters are freed and the minimization carried out, etc. For Bayesian analyses, ADMB uses the MCMC algorithm (Gelman et al. 1995) to estimate the joint posterior probability densities. When posterior densities are presented in this paper they are based on MCMC chains of length 1 million.

Likelihoods

For age composition data, HCAM has two likelihood options. These are the multinomial distribution and a robust-normal distribution (Fournier et al. 1990, Starr et al. 1999). The EASM estimations assume the multinomial distribution and the NASM estimations assume the robust-normal distributions.

For fitting the spawn index data, HCAM only models the lognormal distribution. Both the EASM and NASM analyses assume the lognormal distribution for fitting the spawn index data.

Priors

The priors coded in HCAM are those assumed in the NASM analysis, which include uniform, normal, and lognormal distributions (see Appendix A).

Residuals

To assess deviations from model assumptions we examine two types of residuals; Pearson residuals which express the residual relative to the variability of the observation and normalized

residuals which express the residual on a standard normal scale (see Appendix A for descriptions). For the normalized residuals we calculate two statistics; the standard deviation of the normalized residuals (SNDR) which has an expected value of 1, and a potentially more robust statistic, the median of the absolute residuals (MAR) which has an expected value of 0.67.

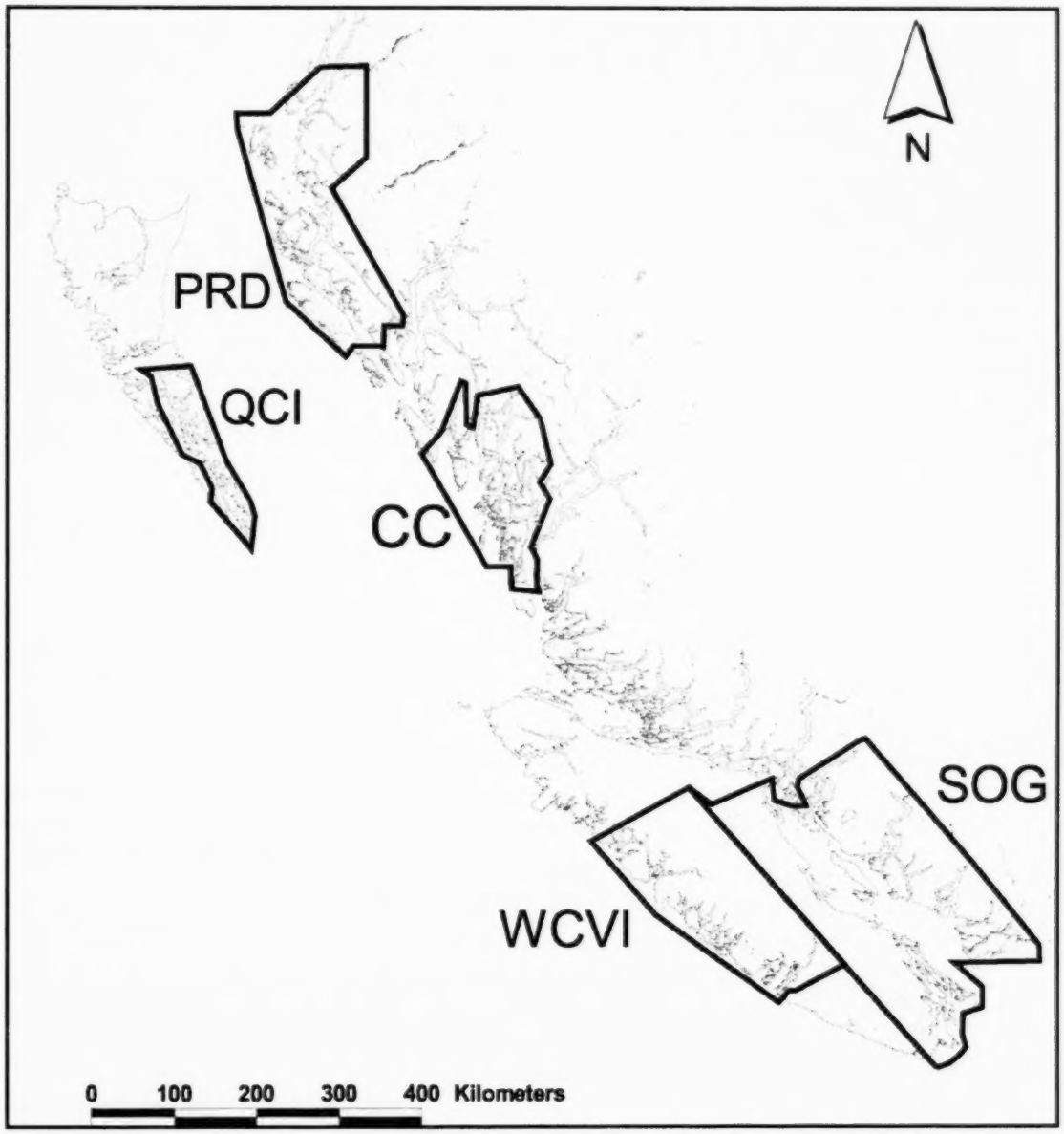

Figure 1. The five major British Columbia herring stock assessment regions: Prince Rupert District (PRD), Queen Charlotte Islands (QCI), Central Coast (CC), west coast of Vancouver Island (WCVI) and the Strait of Georgia (SOG).

RESULTS FROM EASM-EQUIVALENT STOCK RECONSTRUCTIONS

The implementation of EASM that is replicated here is the version described in Schweigert (2005b). The data files used for the 2005 herring stock assessment using EASM (described in Schweigert 2005a) were used for these analyses, so data inputs to the EASM and the HCAM are equivalent. Figure 1 shows the locations of the five herring stocks for which analyses are conducted. Appendix Table 1 describes the parameters estimated in the minimizations.

REPLICATING RESULTS

An EASM-equivalent implementation of HCAM was run for the five herring stocks, and model outputs compared with results from EASM. While EASM results were not replicated exactly, the HCAM results were very close. There were small differences in the value of the total objective function, but there was no pattern of one model obtaining better fits than the other (Table 1). In some cases, one of the models fit was better for all objective function components (eg. GS), and in others there appeared to be a trade-off with both models fitting better to one of the objective function components (eg. WCVI). That pattern suggested the possibility that some of the model fits represented local rather than global minima, so a number of additional HCAM runs were done with different sequences in the phase that specific parameters were included in the estimation. These did not result in any different minima.

Table 1. Values of the objective function and it's components from the EASM and the EASM-equivalent HCAM analyses for the five BC herring stocks.

		Objective Function Value				
Stock	*Model*	*Total*	*Age Composition*	*Catch Data*	*Spawn Index*	*Penalty Function*
GS	*HCAM*	6721.7	5605.8	199.6	382.4	533.8
	EASM	6714.4	5601.4	199.1	380.6	533.3
WCVI	*HCAM*	4943.5	3077.5	280.4	1010.7	574.9
	EASM	4968.8	3141.3	276.3	1011.2	540.0
CC	*HCAM*	4630.5	3257.3	162.8	723.2	487.2
	EASM	4641.4	3261.3	162.9	726.5	490.7
CC[1]	*HCAM*	10719.3	4485.5	412.4	885.8	4935.7
	EASM	10739.7	4501.1	412.5	891.8	4934.4
PRD	*HCAM*	7596.0	6262.2	166.6	751.8	415.4
	EASM	7595.9	6261.5	166.5	751.7	416.2
QCI	*HCAM*	4353.3	2790.0	182.5	587.2	793.5
	EASM	4350.3	2789.2	182.1	586.6	792.4

[1] Central Coast analysis with larger value for penalty function

In the time available, it was not possible to determine why there are small differences between the EASM and EASM-equivalent HCAM fits. One noted difference between the two model implementations was that EASM sets the terminal year age-specific *availability* parameters equal to the geometric mean values of those parameters (mean over final ten years). However, when this option was coded in HCAM the differences between the objective function values did not

improve (more similar for some stocks, but greater differences for others). It appears that there are still minor differences in the two model implementations, but these are unlikely to have a noticeable effect on the results presented here.

Stock reconstructions and parameter estimates are largely indistinguishable between the EASM and EASM-equivalent analyses. Figure 2 shows the ratio of recruitment estimates from EASM relative to those from the HCAM. The ratios are all close to one up to the final two years, where the effect of the two methods for handling the terminal year *availability* parameters is apparent. Note however that when the EASM parameterization of availability was tested in the HCAM, there were still major differences between the recruitment estimates for 2004 and 2005.

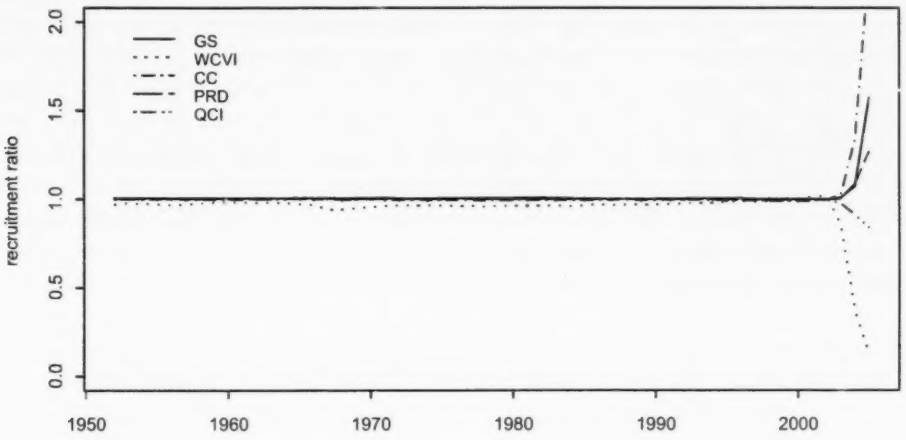

Figure 2. Ratio of recruitment estimates from EASM and HCAM stock reconstructions for the five B.C. herring stocks.

DIAGNOSTICS

Diagnostic features that were examined to assess whether the models provided adequate fits to the data and generated consistent stock reconstructions were the patterns and magnitude of residuals and the retrospective patterns.

Patterns in residuals

For the EASM-equivalent HCAM analyses normalized residuals were calculated for all data components. As discussed previously, the normalized residuals have an expected standard deviation (SDNR) of 1 and an expected median of their absolute values (MAR) of 0.67. Deviation from the expected values indicates inconsistency between the assumed and empirical distribution of residuals and may indicate misspecification of the variances. This could result from model misspecification, underestimating or not accounting for process error, or incorrect estimates of sampling error.

The SDNR and MAR statistics for model fits to the age composition data, the spawn index data and the catch data are shown in Table 2 for the EASM-equivalent analyses. The SDNR statistics

Table 2. Summary statistics for the data fits from EASM-equivalent analyses for the five herring stocks. Reported statistics are the standard deviation of the normalized residuals (SDNR) and the median absolute normalized residual (MAD). Expected values for these statistics are 1 (Std. Dev.) and 0.67 (MAR).

	Age Composition		*Spawn Index*		*Catch*	
Stock	*SDNR*	*MAR*	*SDNR*	*MAR*	*SDNR*	*MAR*
GS	5.88	2.31	3.70	2.52	1.81	0.28
WCVI	4.55	2.18	6.03	2.87	2.61	1.20
CC	4.08	2.09	5.12	3.44	1.92	0.92
PRD	5.45	2.64	5.22	3.38	1.82	0.62
QCI	4.43	2.15	4.62	2.79	2.14	0.39

are substantially greater than 1 for all data sets and stock assessment regions, indicating the magnitude of the residuals are larger than expected given the assumed variances of the data. The MAR statistics are also greater than expected except for the fits to the catch data for a few stocks. When the MAR statistic is smaller than expected and the SDNR statistic is larger than expected there are many small residuals and a few very large residuals. For example, Figure 3 shows the observed and fitted values for the catch data from the GS analysis. The smaller catches are fitted reasonably well while the larger catches tend to be poorly fitted. Given there should not be much information in the data about the true catches, deviations from the observed catches are likely being used to improve fits to other data components (likely the spawn data).

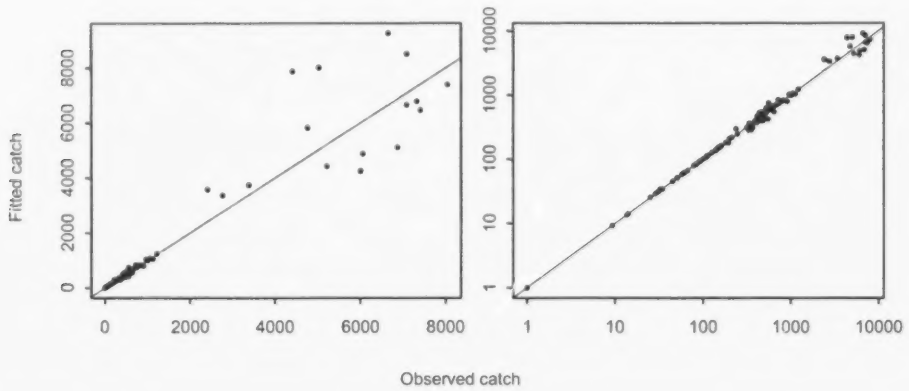

Figure 3. Observed versus fitted catch for the EASM-equivalent analysis of the Strait of Georgia data. The left panel has the data plotted on an arithmetic scale and the left panel has the data plotted on a logarithmic scale.

The EASM model uses maximum likelihood estimation, so misspecification of the variance of the data sets will not affect parameter estimates (and stock reconstructions) if the relative variances are appropriately specified. That is, the same proportional change to all the variance components will result in the same parameter estimates. However, estimates of uncertainty in the free and the derived model parameters (calculated from the Hessian or based on likelihood profiles) will be impacted by the assumed variances. Assuming variances that are smaller than the model fits to the data suggest will result in underestimating the uncertainty in model outputs.

The distributions of residuals for the EASM-equivalent model fits to the fishery age composition data are presented as quantile plots in Figure 4. The quantile plots show the median, the interquartile range and the 10^{th} and 90^{th} quantiles of the residual distributions by age-class and by fishery for each stock assessment region. As already noted, the magnitude of the normalized residuals is inconsistent with the assumed variances of the data (specified as *sample sizes* in the multinomial). More disconcerting, is the pattern in the residuals. In general, the medians and the means of the residual distributions differ markedly from 0. There is no clear pattern to indicate a trade-off in fitting data from the different fisheries (i.e. for an age-class, a preponderance of positive residuals in the fits to one of the fisheries' data balanced by a preponderance of negative residuals in the fits for the other fisheries' data). For the plus age group (7++) the median residuals are negative for most of the stocks and fisheries. These patterns suggest either model misspecification or the influence of a few very large residuals.

Retrospective Analysis

Retrospective analyses were conducted using the EASM-equivalent model to assess whether the stock reconstructions remained stationary as additional years of data become available. Analyses were conducted fitting to the data series with terminal years from 1996 through 2003. As shown in the last herring stock assessment (Schweigert 2005a), there is a strong retrospective pattern for all stocks with abundance estimates decreasing as additional years of data are added (Figure 5).

Taking biomass estimates that result from the full time series (i.e. to 2005) as the best estimates of abundance, we calculate a statistic that measures the change in biomass from the first time it is estimated relative to the "best" estimate (B_y^y, the estimated biomass in year y, as estimated with data through year y and B_y^{2005}, the biomass in year y as estimated with data through 2005). This statistic, presented in Table 3, provides a basis for comparing retrospective patterns among different model formulations. For the EASM analyses these indicate a mean initial estimation "error" of 47.5%. All "errors" are in the direction of overestimating abundance, indicating a persistent bias.

Table 3. Summary statistics for retrospective changes in stock biomass estimates from the EASM-equivalent analyses for the five herring stocks.

	$100\left(B_y^y - B_y^{2005}\right) \Big/ B_y^{2005}$									
Stock	*Mean*	*Mean absolute*	*1996*	*1997*	*1998*	*1999*	*2000*	*2001*	*2002*	*2003*
GS	13.6	13.6	25.5	21.8	7.7	15.1	6.3	13.5	8.3	10.8
WCVI	95.0	95.0	44.0	59.0	126.6	159.0	133.4	82.8	67.7	87.2
CC	33.6	33.6	20.0	22.1	21.3	16.7	33.2	53.4	61.0	41.6
PRD	28.1	28.1	19.4	12.9	16.5	29.9	30.4	48.5	40.3	26.6
QCI	67.2	67.2	46.0	28.7	64.9	67.6	70.4	101.9	83.8	74.4
Mean	47.5	47.5								

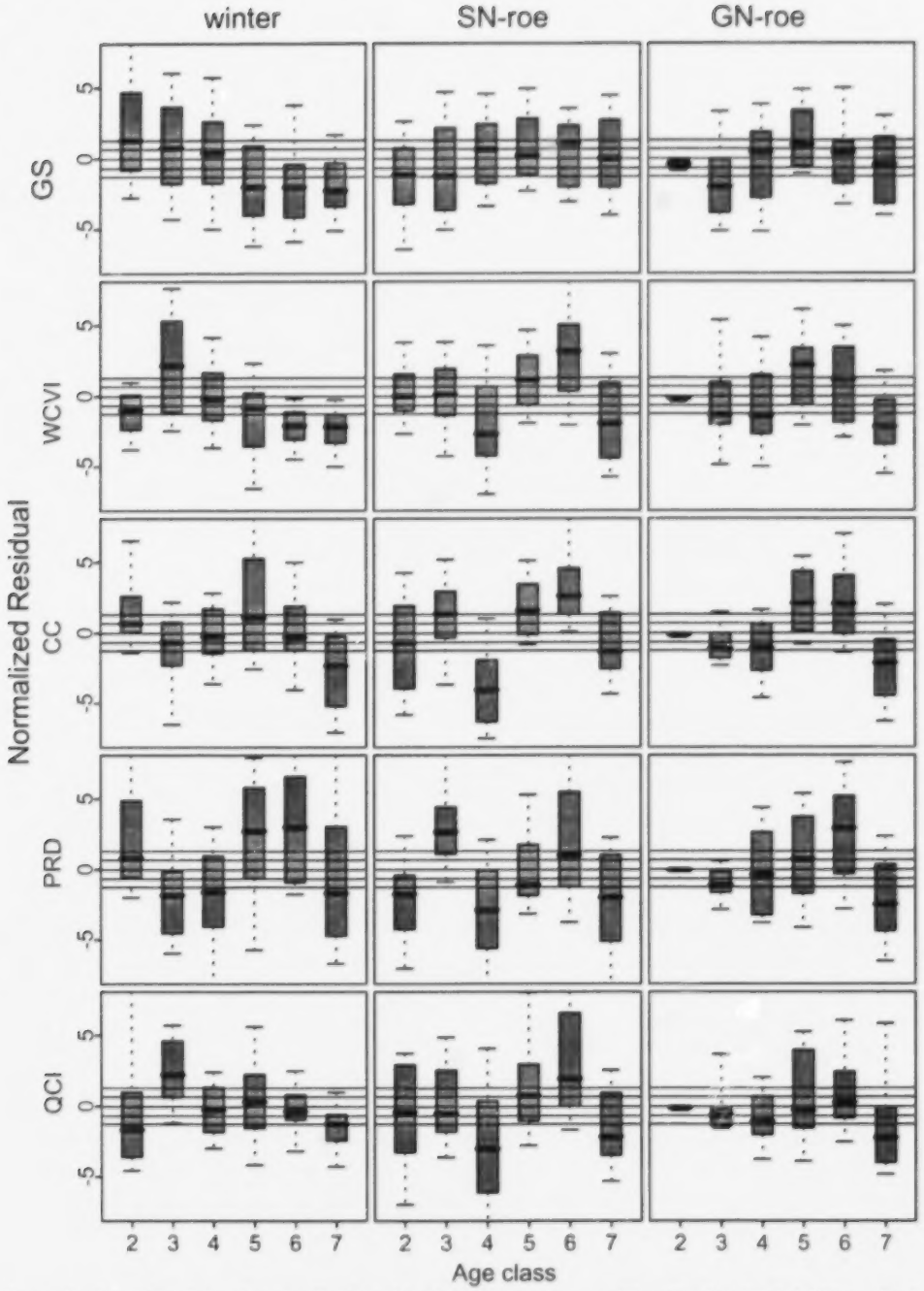

Figure 4. Quantile plots of normalized residuals from age composition fits for the EASM-equivalent model, by fishery and stock. The shaded boxes show the inter-quartile range (with the median shown by the solid bar) and the whiskers show the 10^{th} and 90^{th} quantiles. The horizontal lines indicate the expected values for the 10^{th}, 25^{th}, 50^{th}, 75^{th}, and 90^{th} quantiles.

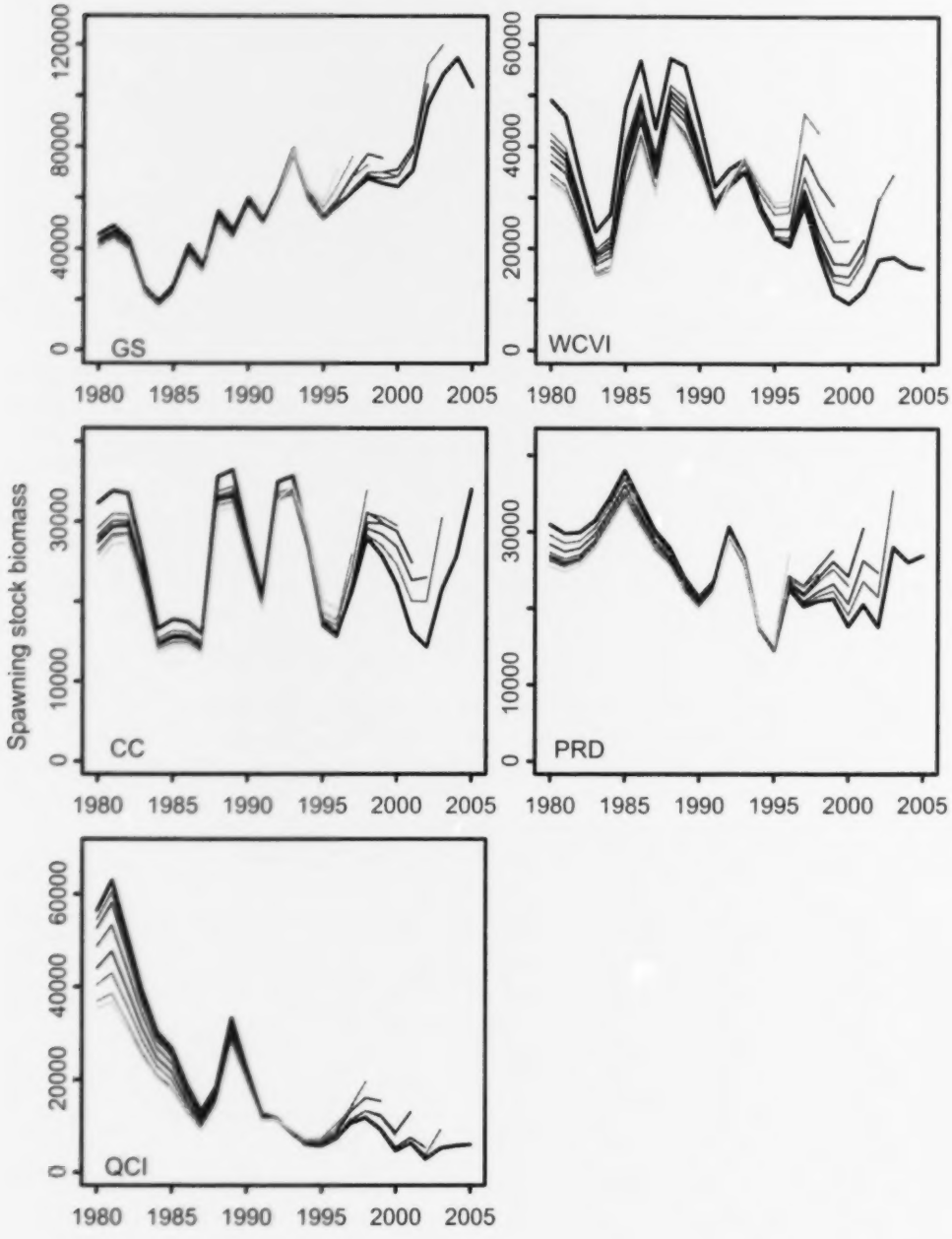

Figure 5. Trajectories of spawning stock biomass for retrospective runs conducted with the EASM-equivalent model and terminal years from 1996 to 2003.

RESULTS FROM NASM-EQUIVALENT STOCK RECONSTRUCTIONS

The NASM structure allows selection among many assumptions, which results in different sets of parameters that are estimated. A number of sets of assumptions were evaluated in an initial paper presenting results of a simulation-estimation study to assess this models' performance (Fu et al. 2004). The different assumptions investigated were time-varying natural mortality rates versus a fixed mortality rate and estimated versus fixed values for the proportionality constant for fitting spawn index data. We replicate the NASM implementation that is described in the current PSARC working paper (Schweigert et al. 2006). The implementation estimates time-varying natural mortality rates and a single proportionality constant for the spawn index data prior to 1988. Appendix Table 1 provides a list of parameters estimated in the NASM-like implementation of HCAM.

Replicating Results

There are some differences between the NASM analyses and the NASM-like version of HCAM that were not resolved, so we do not attempt to replicate outputs from that model. We did not have the data input files from the NASM analyses so we used those from the 2005 EASM herring stock assessment, as we did for the EASM-like implementation of HCAM. The NASM analyses combine the catch and age composition data from the winter and spawning season SN fisheries, and fit to catch in biomass rather than catch in numbers. Because they use different data, there will certainly be differences in analyses from NASM and the NASM-like implementation of HCAM.

Every effort was made to implement the NASM model as described in Schweigert et al. (2006), except for the stock-recruitment likelihood function. We do not allow for estimation of an autocorrelation parameter and use the more traditional likelihood for the stock-recruitment residuals (see Appendix A for details).

Diagnostics

Initial model runs with a NASM-like form of HCAM were conducted using the parameterization described in Schweigert et al. (2006), but not estimating annual natural mortality deviations. Our first model fits were conducted using the robust-normal likelihood for fitting age composition data through all phases of the estimation and using the phase sequence for parameter estimation that is specified in Schweigert et al. (2006). We did additional model runs that used an alternative phasing scheme and also runs where a multinomial distribution was used for fitting age composition data until the final phase of the estimation when the robust-normal was adopted. It has been found (Jim Ianelli, pers. comm.) that when using the robust-normal likelihood for age composition data, better fits are obtained when a multinomial likelihood is used until the final phase of the estimation. Estimates of the total negative log-likelihood at the MPD (mode of the posterior distribution) from this series of model fits indicate that the model minimization often becomes trapped at local minima (Table 4). Given that there appear to be many local minima it is not clear that any of the final fits represents a global minimum.

Table 4. Estimates of the negative log-likelihood (for age composition and spawn index data) and prior contributions to the objective function (for selectivity deviations, natural mortality deviations (M devs), stock-recruitment residuals, sigma R and steepness (h)) for a NASM-like implementation of HCAM using different parameter and likelihood phase-estimation schemes. Function values are at the MPD (mode of the posterior distribution). "C" indicates the robust-normal likelihood for age composition data throughout the estimation; "C/M" indicates using a multinomial likelihood until the final phase when the robust-normal is adopted; "NASM" indicates using the parameter-phase estimation sequencing Schweigert et al. (2006) and "alt" indicates an alternative parameter-phase sequence. The highlighted values indicate the best fits.

		Negative log-likelihoods and contribution of priors to objective function							
Est. scheme	*stock*	*Total*	*Age comp.*	*Spawn data*	*Sel. Devs.*	*M devs*	*S-R resids*	*Sigma R*	*h*
C; NASM	*GS*	324.5	204.2	53.42	65.80	0	-5.24	0.02	0.38
C/M; NASM	*GS*	-43.0	-137.9	40.88	33.23	0	19.49	0.34	0.91
C; alt	*GS*	83.2	1.6	40.51	27.78	0	12.34	0.16	0.78
C/M; alt	*GS*	**-67.3**	-177.0	53.05	33.75	0	21.54	0.54	0.82
C; NASM	*WCVI*	364.6	278.9	47.69	36.94	0	0.12	0.00	0.26
C/M; NASM	*WCVI*	**201.0**	61.0	76.27	36.25	0	25.75	0.76	0.94
C; alt	*WCVI*	392.9	312.5	48.58	17.38	0	13.32	0.23	0.78
C/M; alt	*WCVI*	207.6	60.1	83.62	33.33	0	28.20	1.16	1.26
C; NASM	*CC*	584.0	498.4	44.40	60.19	0	-23.42	0.40	0.39
C/M; NASM	*CC*	**473.1**	278.2	61.75	98.44	0	32.25	1.04	1.17
C; alt	*CC*	459.7	358.0	61.16	39.15	0	0.36	0.00	0.88
C/M; alt	*CC*	517.8	190.3	99.41	59.80	0	143.77	24.13	0.38
C; NASM	*PRD*	770.1	662.6	52.29	67.68	0	-13.06	0.13	0.17
C/M; NASM	*PRD*	527.5	324.9	72.75	100.91	0	27.50	0.93	0.51
C; alt	*PRD*	835.4	723.3	60.17	40.11	0	11.54	0.15	0.08
C/M; alt	*PRD*	**514.8**	315.4	71.09	96.90	0	29.37	1.29	0.70
C; NASM	*QCI*	268.6	143.6	71.62	47.92	0	3.53	0.02	0.11
C/M; NASM	*QCI*	224.5	-6.2	111.85	69.06	0	46.73	2.73	0.33
C; alt	*QCI*	245.6	143.1	62.58	23.98	0	15.17	0.25	0.10
C/M; alt	*QCI*	**213.8**	-8.6	113.93	55.75	0	47.97	3.68	0.86

Using a multinomial error structure for fitting the age composition data in the initial phases of the estimation and then switching to the robust-normal error structure in the final phase consistently produced lower minima than were obtained using the robust-normal through all phases of the estimation. Using this approach resulted in better fits to the age composition data and larger contributions to the objective function from the prior on the stock-recruitment residuals and sigmaR (the variance of the stock-recruitment residuals parameter). In terms of the preferred sequence for including parameters in the estimation, neither of the two schemes evaluated generated consistently better fits. Further analyses looking at alternative phasing schemes may produce a sequence that consistently produces the best fits.

Because NASM is structured for Bayesian estimation, the inability of the estimation to consistently find a global minimum, may not be of issue. That is, if the same joint posterior distributions are estimated from different MPD starting points, the local minima are not of concern. We did not investigate if this was the case because of computing limitations, but suspect that there would be differences in the joint posterior distributions given different starting

points for the MCMC chain (ADMB begins the MCMC chain at the estimated MPD and uses the estimated covariance matrix at the MPD to determine chain steps).

The next step in implementing the NASM-like model was to estimate the natural mortality deviation parameters. For these runs we used the combination multinomial/robust-normal age composition likelihoods and the NASM phase sequence for estimating parameters. Being aware of local minimum concerns, a number of runs were conducted for each stock assessment region with different initial values for natural mortality. That is, the natural morality rate was fixed at different values until phase 4, where the natural mortality deviations were estimated. The estimated values of the objective function and the range in the annual natural mortality estimates are shown in Table 5 for the various runs.

Table 5. Estimates of the negative log-likelihood and prior contributions to the objective function for a NASM-like implementation of HCAM that estimates annual natural mortality rates. Estimated natural mortality rates include the mean, the minimum and the maximum values. Function values are at the MPD (mode of the posterior distribution). Results are presented for runs that had different values of M in the initial phases of the analysis (0.45, 0.65, 0.25, and estimated), and the best fit for each stock is highlighted.

		Natural Mortality			*Negative log-likelihoods and contribution of priors to objective function*							
Est. sch.	*Stock*	*Mean*	*Min*	*Max*	*Total*	*Age comp.*	*Spawn data*	*Sel. Devs.*	*M devs*	*S-R resids*	*Sigma R*	*h*
0.45	*GS*	0.51	0.39	1.08	-57.4	-167.11	38.87	31.72	21.48	16.12	0.23	1.24
0.65	*GS*	0.56	0.43	0.93	-55.4	-140.02	28.88	30.48	18.58	5.79	0.02	0.85
0.25	*GS*	0.58	0.40	1.79	-7.7	-146.35	40.25	32.83	36.56	17.50	0.25	1.84
est	*GS*	0.55	0.43	0.75	**-90.8**	-186.44	37.95	33.12	15.06	9.04	0.09	0.35
0.45	*WCVI*	0.48	0.34	0.69	190.7	60.19	53.73	33.61	19.61	21.14	0.50	1.88
0.65	*WCVI*	0.47	0.32	0.71	**169.9**	40.92	54.72	34.14	21.49	16.86	0.35	1.42
0.25	*WCVI*	0.48	0.34	0.64	183.0	49.81	53.40	33.74	17.07	26.12	0.95	1.92
est	*WCVI*	0.47	0.34	0.67	174.3	57.50	51.11	34.60	15.97	14.10	0.24	0.77
0.45	*CC*	0.29	0.22	0.49	**338.8**	164.03	75.17	58.19	16.27	22.62	0.61	1.92
0.65	*CC*	0.25	0.20	0.41	353.5	183.82	75.15	55.20	12.86	23.82	0.60	1.91
0.25	*CC*	0.28	0.24	0.46	345.6	172.11	71.81	59.51	12.87	26.05	0.99	1.92
est	*CC*	0.27	0.21	0.42	356.3	180.05	81.01	53.82	13.46	25.08	1.04	1.82
0.45	*PRD*	0.28	0.24	0.37	**469.9**	278.67	60.70	96.33	7.81	24.84	0.70	0.53
0.65	*PRD*	0.27	0.23	0.36	472.3	279.43	65.91	92.94	6.13	26.29	0.89	0.35
0.25	*PRD*	0.29	0.24	0.39	474.1	274.48	60.41	99.20	5.98	31.32	1.19	1.23
est	*PRD*	0.27	0.23	0.35	471.8	284.44	57.22	101.95	4.51	22.58	0.72	0.02
0.45	*QCI*	0.53	0.36	0.87	**154.8**	-54.47	75.70	70.20	18.31	41.86	2.59	0.56
0.65	*QCI*	0.55	0.40	0.92	155.4	-49.93	69.46	70.86	18.56	43.87	2.33	0.21
0.25	*QCI*	0.54	0.37	0.88	171.7	-39.29	76.92	67.88	18.47	43.74	2.92	1.07
est	*QCI*	0.43	0.31	0.70	162.1	-54.10	82.99	68.75	16.03	45.42	2.79	0.16

There is no pattern where one estimation scheme (initial M value) consistently results in better fits. In general, it appears that better fits are obtained to both the age composition data and the spawn index data when annual natural mortality rates are estimated (compare values in Tables 4 and 5). We do not attempt statistical tests to determine if the improvements in model fit under the "time-varying natural mortality rates" hypothesis are significant because for a Bayesian

estimation based model this would require estimating the joint posterior distributions for all model runs to calculate "Bayes Factors" (Kass and Raftery 1995).

The estimated annual natural mortality rates for the five herring stocks are shown in the left panels of Figure 6. The range in natural mortality rates we estimated is much lower than the range reported by Fu et al. (2004, their figures 8,11,14,17 and 20). There are two factors that may cause this difference: 1) not using the robust normal age composition likelihood through all estimation phases, and 2) the prior on the natural morality deviation parameters having less effect on the estimation because we are fitting to more age composition data (for three fisheries rather than two). To investigate these factors we first calculated annual natural morality rates for runs where we use the robust normal age composition likelihood through all phases of the estimation. This resulted in higher average natural mortality rate estimates for the CC and PRD stocks, though the variation in M did not increase. Then we increased the standard deviation of the natural mortality deviation prior (from 0.2 to 0.3). This resulted in annual estimates of natural mortality that were more similar to those obtained by Fu et al. (Figure 6, right panels).

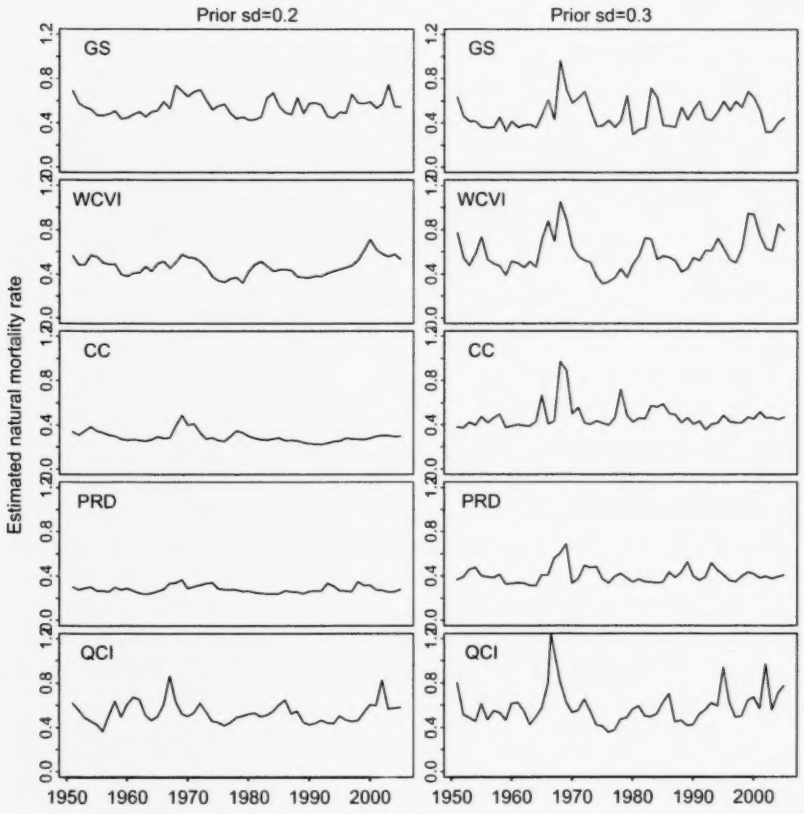

Figure 6. Estimates of annual natural morality rates from the NASM-like analyses for the five herring stocks. The left panels show results from runs with the NASM natural mortality deviation prior and the right panels show results from runs with a higher natural mortality deviation prior.

Patterns in residuals

Statistics summarizing the residuals from the fits to the age composition data and the spawn index data are shown in Table 6 for the NASM-like implementation of HCAM. The residual estimates are from the best fits obtained when estimating annual natural mortality rates (Table 5). For the age composition fits, we present statistics for both Pearson residuals and the approximate-normalized residuals because the robust-normal likelihood used for those data does not have exact normalized residuals. The Pearson residuals provide a basis for evaluating the effect of using the robust-normal likelihoods in discounting data outliers.

The SDNR and MAR statistics indicate that the model is over-weighting both the spawn index data and the age composition data. The SDNR for the age composition Pearson residuals is quite large relative to the SDNR of the approximate-normalized residuals suggesting there is a large effect of the robust-normal likelihood in discounting larger residuals. The residual statistics indicate there is greater deviation from the model specification than expected based on the assumed variances of the data.

Table 6. Summary statistics for Pearson and normalized residuals for fits to age composition and spawn index data for the NASM-like model runs. Reported statistics are the standard deviation of the normalized residuals (SDNR) and the median absolute normalized residual (MAD). Note that for the age composition fits of the normalized residuals are only approximate . Expected values for these statistics are 1 (SDNR) and 0.67 (MAR).

	Age Composition				*Spawn Index*	
	Pearson residuals		*Normalized residuals*		*Normalized residuals*	
Stock	*SDNR*	*MAR*	*SDNR*	*MAR*	*SDNR*	*MAR*
GS	5.86	0.79	1.66	0.79	1.18	0.73
WCVI	5.03	1.03	1.80	1.03	1.39	0.90
CC	10.47	1.09	1.84	1.09	1.64	0.93
PRD	7.37	1.17	1.87	1.17	1.49	0.94
QCI	7.68	0.82	1.70	0.82	1.66	1.19

The distributions of normalized residuals for the model fits to the fishery age composition data are presented as quantile plots in Figure 7. As noted, the magnitude of the normalized residuals are inconsistent with the assumed variances of those data, though to a lesser extent than for the EASM-like model. There is a general pattern, in particular in the fits to the SN roe fishery data, for primarily negative residuals in the fits for the younger and older age classes and positive residuals in the fits for the intermediate age-classes. This pattern suggests an inconsistency in the model structural assumptions and the age composition data.

Retrospective Analysis

Retrospective analyses were conducted using the NASM-like model to assess whether the stock reconstructions remained stationary as additional years of data become available. Analyses were conducted fitting to the data series with terminal years from 1996 through 2003. We calculated the same statistics as for the EASM-like model to measure the degree to which biomass estimates change as additional years of data are added to the estimation. Results are shown in Table 7.

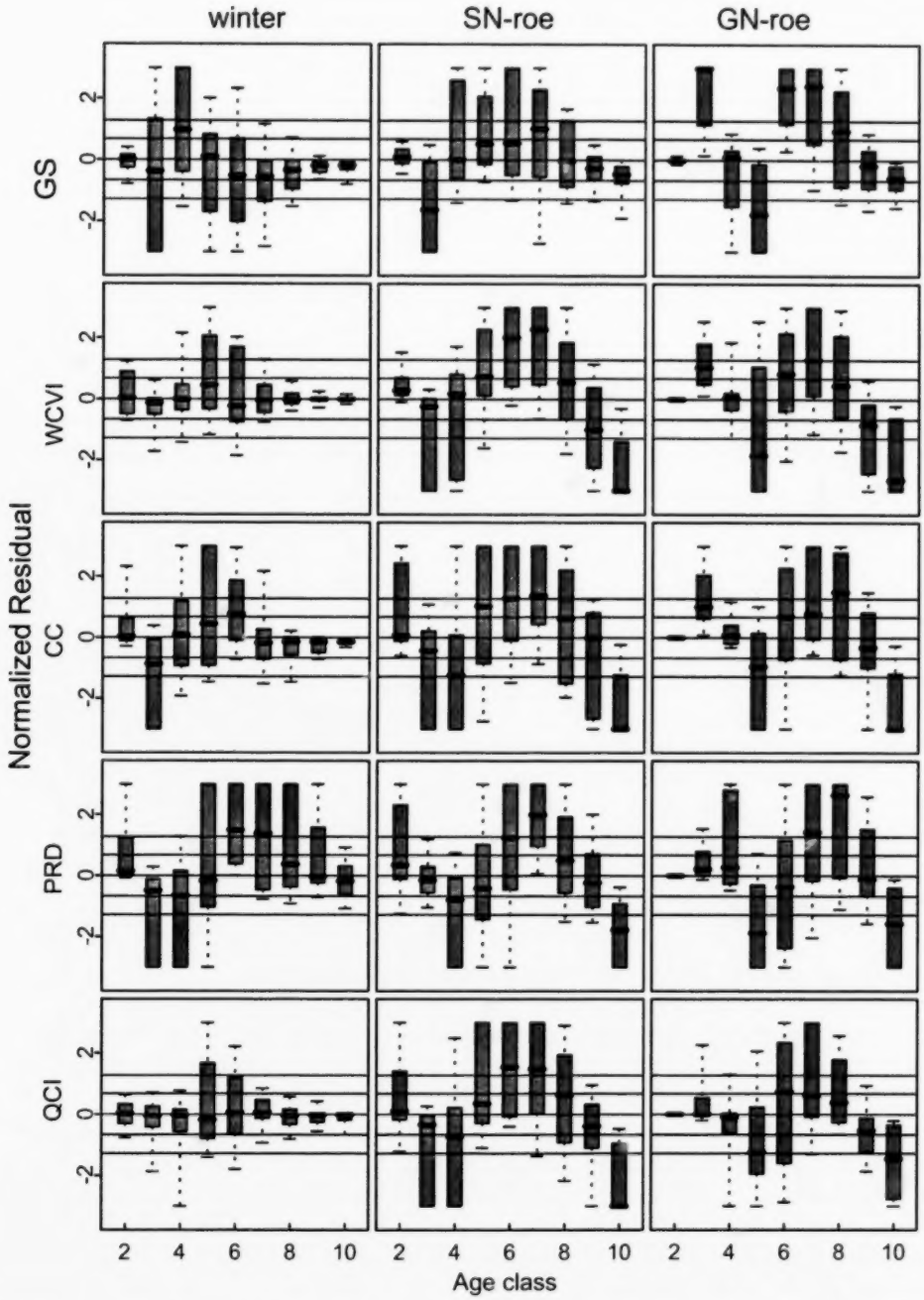

Figure 7. Quantile plots of normalized residuals from age composition fits for the NASM-equivalent model, by fishery and stock. The shaded boxes show the inter-quartile range (with the median shown by the solid bar) and the whiskers show the 10th and 90th quantiles. The horizontal lines indicate the expected values for the 10th, 25th, 50th, 75th, and 90th quantiles.

Table 7. Summary statistics for retrospective changes in stock biomass estimates from the NASM-like model analyses for the five herring stocks.

			$100\left(B_y^y - B_y^{2005}\right) \Big/ B_y^{2005}$							
Stock	*Mean*	*Mean absolute*	*1996*	*1997*	*1998*	*1999*	*2000*	*2001*	*2002*	*2003*
GS	43.2	43.2	15.7	20.8	98.8	11.0	8.4	75.3	28.4	87.2
WCVI	51.0	52.0	-4.1	9.3	46.5	111.9	95.8	41.5	43.4	63.7
CC	-8.6	14.0	-6.0	-37.7	-22.0	-17.7	-7.1	18.4	0.3	3.0
PRD	8.7	18.9	-28.1	-12.8	26.2	13.7	13.7	42.0	2.8	12.0
QCI	16.2	28.5	-13.0	-22.9	48.2	22.4	4.0	87.8	-13.3	16.2
Mean	22.1	31.3								

The retrospective patterns from the NASM-like model are much better than those from the EASM-like model. Although this model also tends to initially estimate higher abundance than what later, more mature data series suggest, this tendency does not hold across all stocks and for all years. Overall stocks and years, the mean percent "error" in the initial abundances estimates is 22.1% and the mean absolute percent "error" in the initial abundance estimates is 31.3%. This compares with a mean percent "error" and a mean percent absolute "error" of 47.5% for the EASM-like model.

Because the NASM is structured for Bayesian estimation, a more appropriate retrospective analysis would be to estimate the full joint posterior distribution for each of the retrospective years and then see how the distributions of stock biomass change as additional years of data are added to the model. This was not feasible because of computing limitations, and we only estimated the joint posterior distributions for the full data sets. The marginal posterior distributions of spawning stock biomass (the 10^{th} and 90^{th} percentiles) are shown in Figure 8 along with the retrospective spawning stock biomass estimates. In general, the retrospective abundance trends are within the 10^{th} and 90^{th} percentiles of the marginal posterior distributions from the analysis using the full (through 2005) data set.

DEVELOPING A HCAM FORMULATION FOR PACIFIC HERRING

In this section we describe a step-wise process to evaluate alternative parameterizations and assumptions with the objective of obtaining a consistent analysis of the herring data. Where possible we use objective criteria to evaluate model performance between competing assumptions. We do not conduct hypothesis tests to select among model formulations, because with Bayesian estimation this would require calculating the joint posterior distribution for all model runs (Kass and Raftery 1995) and that is beyond the limits of available computing power. Rather we look for consistency in improvement in model fits across stocks, and focus on the patterns in model residuals. For the higher parameter models, we expect to get reasonable patterns in the residuals.

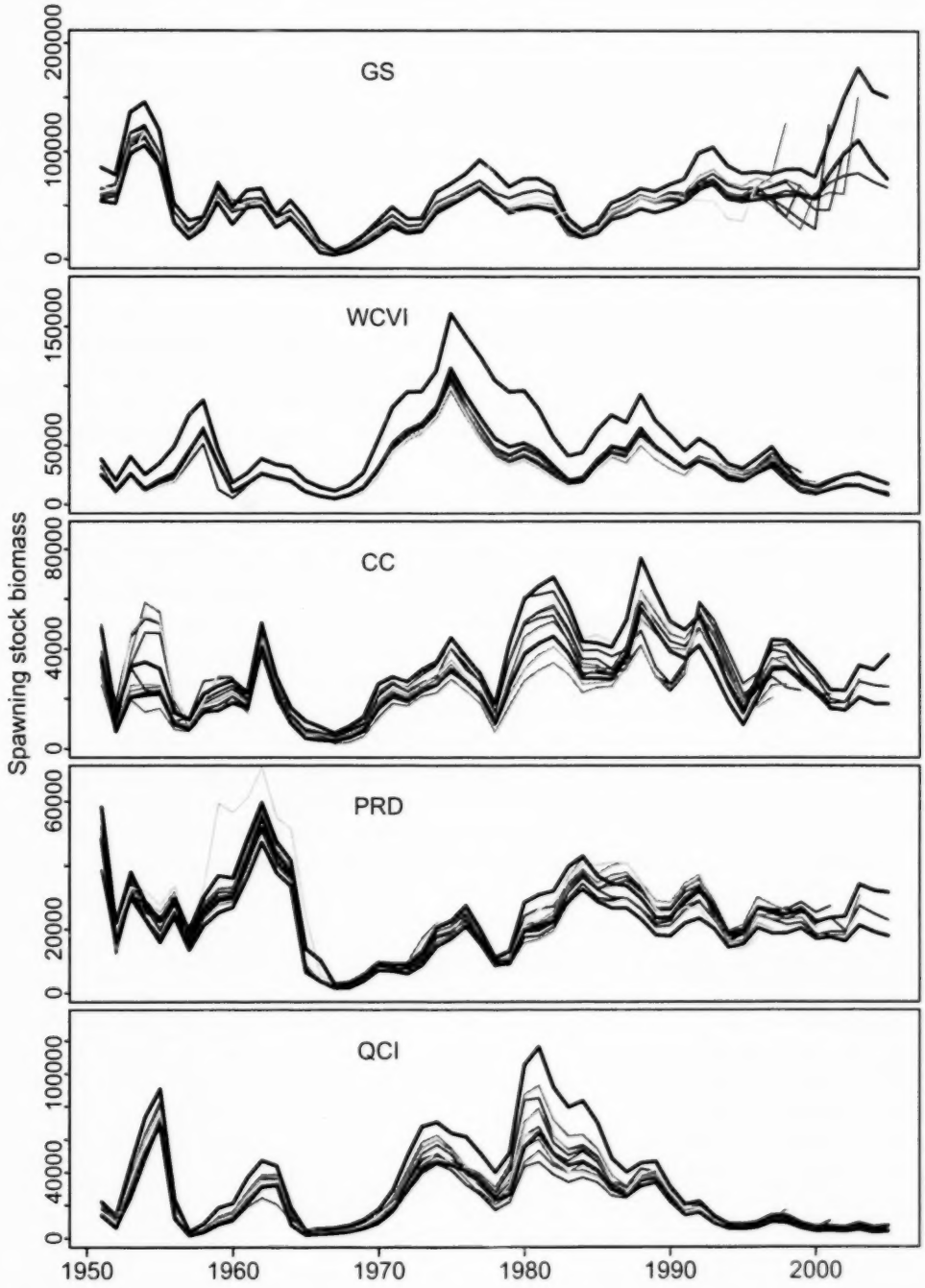

Figure 8. Estimates of spawning stock biomass from retrospective analyses (1996-2003, light coloured lines) and marginal posterior estimates (using data through 2005, 10th and 90th percentiles of the distribution are shown as heavy lines). Results are from the NASM-like implementation of HCAM.

BAYESIAN ESTIMATION

We choose Bayesian estimation for these analyses. The Bayesian approach is the state-of-the art in fisheries modelling because it allows estimation of uncertainty in both estimated and derived model parameters (Punt and Hilborn 1997). Most of the results we present are based only on MPD estimates because computer limitations restrict the number of joint posterior distributions that can be estimated. Consequently, results and their interpretation may be biased, because often MPD parameter estimates are close to the bounds of their marginal posterior values.

Assumptions made about priors can significantly impact results, so efforts to develop informed priors either from data that are not used in the model or from published meta-analysis would be of value. The prior assumptions used in the following analysis are either taken from the NASM analysis or are *ad hoc*. Appendix A and Appendix Table 2 describe the priors and Appendix Table 1 lists the parameters estimated in each of the runs.

To ensure that model priors have the appropriate influence in the analyses, it is important that the weighting given to the data (i.e. variance assumptions) is consistent with the ability of the model to fit the data. Commonly used methods to ensure appropriate data weighting include: iterative re-weighting of data components (Cope and Punt 2006, Helser et al. 2004); estimating process error variance for some or all data components (Bull et al. 2003, Francis 2006); estimating an overall variance term that is added to the individual variance components (Kim et al. 2003), or using concentrated likelihoods (Sullivan et al. 1999, Otter Research Ltd. 2000). For these analyses we assume (rather than estimate) process error in fitting to the age composition data, and increase the assumed variance of the spawn index data (from that assumed in the NASM analyses). Table 8 shows the means of the actual age composition sample sizes, as used in the EASM and NASM-like model implementations, and Figure 9 shows the rescaling of actual samples size to effective samples sizes for the HCAM model runs where process error is included.

Table 8. Average age composition samples sizes by stock and fishery.

	Average age composition sample size		
	Winter	*Sn-Roe*	*GN-Roe*
GS	3112	6282	911
WCVI	1247	5268	531
CC	1962	5261	839
PRD	1601	3206	676
QCI	603	2691	353

STRUCTURE OF THE INITIAL HCAM MODEL

The model structure for our initial runs is similar to the NASM parameterization, though simplified in some respects. The model is parameterized as follows:

- Uses the discrete form of the catch equations. Assumes catch is known without error.

- Models three fishing periods (for the winter, spawning season SN, and spawning season GN) with fractions of the total mortality in each period (0.45, 0.45, and 0.10). Because the discrete form of the catch equations have natural mortality occurring prior to fishing mortality this sets 90% of the annual natural mortality prior to the spawning season.
- Age-based logistic selectivity function, with common selectivity parameters for the winter and spawning season SN fisheries. No fishery specific selectivity deviations estimated.
- Population initialized at equilibrium in 1943, and assume no catch taken until 1951. Plus group at age 10.
- Natural mortality rate estimated with normal prior as specified in Appendix A.
- Assume the Beverton-Holt stock recruitment relationship.
- Multinomial distribution for fitting age composition data and lognormal distribution for fitting spawn index data. Assume process error in the fit to age composition data and set to a fixed value. The assumed variance of the fit to spawn index data is increased from the values used in the NASM analyses.

From this initial model structure (termed R1), additional analyses are conducted that change one model component at a time. Appendix Table 1 describes the parameters estimated in each set of runs, Table 9 presents summary statistics for the various runs, and Appendix Table 3 presents estimates of all components of the objective function for each of the runs.

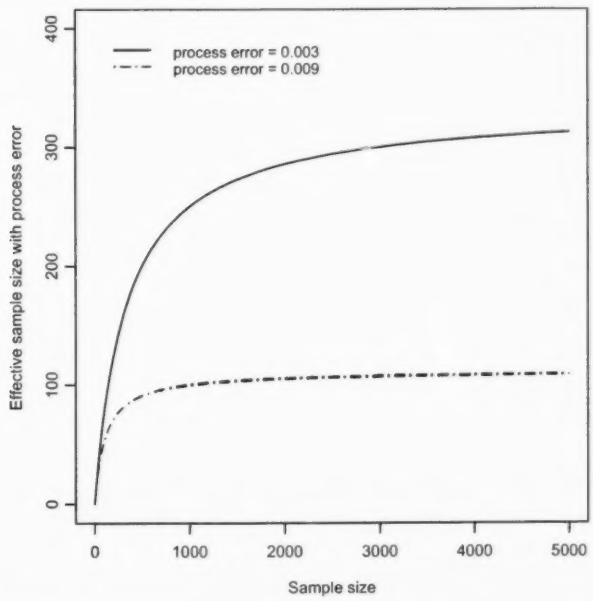

Figure 9. The relationship between actual sample size and effective sample size when process error is included in the estimation. All HCAM model runs assume the 0.003 process error, except for R13 where the 0.009 process error is assumed.

HCAM ANALYSES

Run R1

Figure 10 shows the mean normalized residuals for the R1 fits to age composition data for each age-class, fishery and stock. There is an over-riding pattern of negative residuals for the fits for the younger age-class, positive residuals for the fits for the intermediate age-classes, and negative residuals for the fits to the oldest age-class. This pattern is captured in a "mean of means" statistic that calculates the mean of the age-specific means across the fisheries and stocks, and provides a convenient way to compare the over-all residual patterns across model runs (Table 10).

Model fits to the age composition data and the spawn index data are considerably worse than expected, given the assumed variances of these data. That is, the normalized residuals statistics, the SDNR and the MAR, are greater than their expected values for all data sets (Table 9). Additionally, the autocorrelations in the spawn index residuals indicate there are reasonably strong patterns in the lack of fit to the spawn index data (Table 9). The objective of increasing the model complexity in the following series of model runs is to reduce the magnitude and patterns in the residuals.

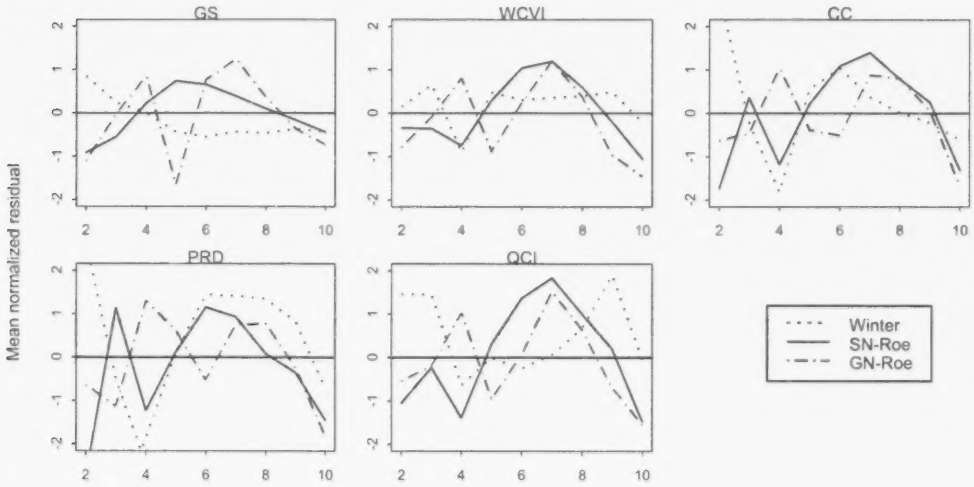

Figure 10. Mean normalized residuals for the R1 fits to age composition data by age-class fishery and stock.

Table 9. Summary statistics for the HCAM series of model runs (R1-R14) for the five herring stocks. Statistics include the objective function value (F), the standard deviation of normalized residuals (SDNR) , the median absolute normalized residual (MAR), the autocorrelation (AC) in the spawn index residuals, and the number of parameters estimated in the minimization (NVAR).

Stock	*Statistic*	*R1*	*R2*	*R3*	*R4*	*R5*	*R6*	*R7*	*R8*	*R9*	*R10*	*R11*	*R12*	*R13*	*R14*
GS	*F*	1265.0	1173.7	1263.8	1100.1	1085.1	1014.8	1073.5	1055.7	997.8	983.6	398.1	388.6	404.3	-613.3
WCVI	*F*	1141.3	1153.0	1089.2	1064.8	1041.7	879.7	1005.3	911.9	861.1	856.5	400.6	392.1	389.0	-338.6
CC	*F*	1482.1	1473.3	1322.9	1234.2	1214.8	999.7	1148.2	1028.1	955.5	944.5	578.9	572.4	460.9	-368.6
PRD	*F*	2653.9	2610.1	2431.8	2249.9	2200.5	1858.5	2142.3	1979.8	1983.0	1965.5	886.4	862.3	892.2	-77.9
QCI	*F*	1576.5	1655.0	1502.4	1506.6	1484.6	1173.1	1410.1	1314.6	1148.9	1141.4	590.6	583.0	606.3	-153.1
Age composition															
GS	*SDNR*	1.63	1.58	1.63	2.41	1.50	1.80	1.59	1.57	1.51	1.51	0.94	0.94	0.98	1.26
	MAR	0.87	0.81	0.87	0.76	0.76	1.10	0.84	0.86	0.84	0.84	0.58	0.56	0.55	0.66
WCVI	*SDNR*	1.93	1.89	1.85	1.93	1.86	2.18	1.93	1.89	1.87	1.87	1.12	1.11	1.24	1.27
	MAR	1.06	1.04	1.01	0.95	0.94	1.10	1.01	0.96	0.94	0.93	0.56	0.57	0.58	0.69
CC	*SDNR*	2.10	2.15	2.01	1.98	1.96	2.20	2.02	1.87	1.79	1.79	1.29	1.28	1.20	1.27
	MAR	1.06	1.04	1.00	0.93	0.92	1.02	0.95	0.85	0.88	0.87	0.69	0.69	0.60	0.65
PRD	*SDNR*	2.85	2.83	2.84	2.58	2.53	2.89	2.66	2.57	2.95	2.95	1.65	1.63	1.90	1.56
	MAR	1.39	1.32	1.41	1.31	1.27	1.61	1.37	1.36	1.40	1.41	0.90	0.87	0.92	0.91
QCI	*SDNR*	3.01	2.75	3.77	3.56	2.92	2.81	3.00	2.67	3.20	2.95	1.51	1.51	2.48	1.41
	MAR	1.23	1.23	1.07	1.14	1.17	1.23	1.21	1.12	1.11	1.41	0.82	0.81	0.76	0.75
Spawn Data															
GS	*SDNR*	1.23	1.25	1.22	1.27	1.27	1.29	1.28	1.30	1.17	1.06	0.92	0.83	0.95	1.04
	MAR	0.85	0.80	0.84	0.86	0.80	0.85	0.80	0.85	1.00	0.76	0.62	0.42	0.64	0.64
WCVI	*SDNR*	1.41	1.58	1.39	1.49	1.51	1.51	1.52	1.52	1.09	1.09	0.99	0.97	0.98	0.99
	MAR	1.01	1.03	0.97	1.18	1.12	1.06	1.13	0.95	0.71	0.64	0.59	0.59	0.60	0.66
CC	*SDNR*	1.40	1.64	1.50	1.48	1.48	1.46	1.51	1.40	1.27	1.21	1.24	1.21	1.16	1.23
	MAR	0.96	0.94	1.26	1.12	1.12	1.03	1.10	0.92	0.77	0.69	0.68	0.64	0.72	0.62
PRD	*SDNR*	1.22	1.34	1.46	2.34	2.36	2.15	2.34	1.74	1.33	1.24	1.11	1.08	1.15	1.06
	MAR	0.63	0.86	1.10	1.76	1.77	1.48	1.70	1.32	0.56	0.54	0.66	0.62	0.45	0.60
QCI	*SDNR*	1.83	2.40	2.30	2.32	2.35	1.93	2.33	1.89	1.44	1.42	1.28	1.26	1.37	1.42
	MAR	1.01	1.05	1.75	1.57	1.65	1.29	1.68	1.24	0.70	0.76	0.93	0.88	0.72	0.81
GS	*AC*	0.49	0.49	0.48	0.51	0.52	0.53	0.52	0.54	0.52	0.46	0.21	0.09	0.25	0.32
WCVI	*AC*	0.66	0.59	0.67	0.72	0.74	0.73	0.74	0.70	0.54	0.52	0.40	0.37	0.46	0.46
CC	*AC*	0.42	0.29	0.50	0.45	0.45	0.47	0.47	0.50	0.38	0.34	0.27	0.24	0.31	0.31
PRD	*AC*	0.12	0.18	0.41	0.72	0.72	0.69	0.72	0.57	0.29	0.20	0.09	0.04	0.08	-0.15
QCI	*AC*	0.28	0.56	0.61	0.61	0.61	0.39	0.60	0.35	0.02	0.00	0.10	0.08	0.01	0.03
	NVAR	71	71	74	74	76	74	76	77	132	133	211-252	212 - 253	132	132

Table 10. Mean (across fisheries and stocks) of the mean residuals for the fit to the age composition data by age-class. Note that the terminal age-class is always a 'plus' group.

Model	Age-class								
Run	2	3	4	5	6	7	8	9	10
R1	-0.18	0.00	-0.34	-0.06	0.48	0.87	0.50	0.01	-1.00
R2	0.05	-0.01	-0.50	0.08	0.37	0.73	0.41	-0.07	-1.00
R3	-0.07	-0.24	0.22	-0.30	-0.05	0.62	0.55	0.27	-0.77
R4	0.09	-0.22	-0.11	-0.01	0.04	0.43	0.44	0.31	-0.45
R5	0.05	-0.25	-0.12	0.01	0.05	0.41	0.37	0.10	-0.57
R6	0.10	-0.20	-0.12	0.19	0.31	-0.14			
R7	0.04	-0.26	-0.12	0.04	0.09	0.44	0.24	-0.35	
R8	0.04	-0.18	0.03	0.08	-0.10	0.14	0.19	-0.13	
R9	-0.07	-0.22	0.01	0.07	0.01	0.21	0.33	0.09	
R10	-0.06	-0.22	0.02	0.06	0.00	0.20	0.33	0.11	
R11	-0.01	-0.16	0.04	0.01	-0.08	0.21	0.21	-0.12	
R12	-0.01	-0.16	0.05	0.00	-0.08	0.22	0.21	-0.16	
R13	-0.05	-0.14	-0.01	0.04	-0.01	0.12	0.21	0.07	
R14	-0.14	-0.82	-0.37	-0.24	-0.07	0.18	0.23	-0.15	

Run R2

Run R2 differs from run R1 in that availability parameters are estimated and selectivity of the winter and seine roe fisheries are set to 1 (i.e. all available fish are equally selected). Additionally, with this formulation all available fish are assumed to be mature and spawning and the input maturity ogive is not used to estimate spawning abundance. The availability parameterization was originally used in the herring catch-age model (eg. EASM) because that model was based on the instantaneous (Baranov) catch equations. With the instantaneous form of catch equations all fish in an age-class whose selectivity is non-zero are potentially vulnerable, and with high fishing mortality rates as seen during the "reduction" fishery, are potentially caught in the fishery. The availability parameterization allows a reserve of younger fish that are not vulnerable to the fishery. The discrete form of the catch equations accomplishes the same objective, ensuring that the non-selected proportion of an age-class is invulnerable to the fishery. As such, the distinction between the availability and selectivity formulations should not make much difference in model fitting.

The availability parameters are modelled with a logistic function so this parameterization does not change the number of "free" parameters estimated through the minimization. Comparison of the R1 and the R2 runs show equivocal results. For three of the five stocks the R2 fits are better as a result of improvements in fits to the age composition data (Table 9 and Appendix Table 3). For all but one stock, the fits to the spawn data are worse for the R2 runs. The age composition residual patterns appear equally bad for runs R1 and R2 (Table 10), and although the autocorrelation in the spawn index residuals changes substantially for 3 of the 5 stocks, the changes do not favour one model over the other. There is no clear basis for selecting one parameterization over the other. We've chosen to retain the selectivity parameterization because it allows fishery dependent changes (deviations) in selectivity whereas the availability parameterization allows only annual changes in the availability parameters.

Run R3

Model runs R3 adopt the structure of the R1 runs, except that the logistic function used to describe the form of age specific selectivity for the seine fisheries is replaced with direct estimates of selectivity parameters for age-classes 2 through 6. Selectivity of age-classes 7 and older is fixed at 1. This increases the number of parameters in the model by 3.

With this alternative parameterization of age-specific selectivity for the seine fisheries the objective function decreased for all stocks, in some cases by a considerable amount (Table 9). The improvements in model fit are all obtained through better fits to the age composition data and in general the fits to the spawn index data are worse. For the PRD and the QCI stocks the autocorrelation in spawn index residuals increases substantially (Table 9). The patterns in age composition residuals are slightly better (Table 10) but still show strong age related trends. Because of the improvements in fit and slight improvement in age composition residual patterns, we choose to retain the age specific parameters rather than the logistic function for describing selectivity.

Run R4

The R4 set of model runs follow from the R3 set of runs with the logistic age-based selectivity function replaced by a size-based logistic function for the GN fishery. This alternative parameterization does not change the number of parameters in the model.

Using the size-based selectivity model rather than the age-based selectivity model for the GN fishery substantially improves the model fits for all stocks except for QCI where there is a slightly poorer fit (Table 9). Improvements in overall model fit generally result from improvements in the fit to the age composition data, and for the PRD stock there is a substantial decrease in the fit to the spawn index data (Appendix Table 3). The patterns in the age composition residuals are generally better (Table 10) though the overall age related pattern remains. There appears to be strong support in the data for the size-based selectivity parameterization (except for QCI), and we retain this parameterization.

Runs R5 to R7

In age-structured fisheries models a "plus" group (a terminal age-class that accumulates all fish at or older than the "plus" age) is often used to deal with ageing error. The idea is that ageing errors increase with age, and grouping the older fish will decrease the influence of ageing errors. An alternative approach, or perhaps one that can be used in conjunction with a plus group, is to explicitly allow for ageing error. This can be done by providing an ageing precision matrix to the model, which is then used to modify the fitted age compositions. Ageing precision matrices are estimated from duplicate ageing of age structures, and by necessity assume that ageing error is symmetrical. We chose a different approach, estimating an ageing error matrix based on the assumption that for each annual ring in the ageing structure, there is a probability p that the ring will not be counted and a probability q that two rings will be counted (see Appendix A for description).

With the R5 and R6 set of model runs we explore using a lower "plus" group and estimating ageing errors in the model estimation. The R5 model runs have the same structure as the R4 runs, except that ageing error is estimated. This increases the number of estimated parameters by 2.

All stocks show a moderate improvement in their fits with the inclusion of the ageing error parameters (Table 9). The improvements are primarily obtained with better fits to the age composition data, though the over-riding residual patterns do not improve much (Table 10). The estimated values for the ageing error parameters are shown in Table 11. There is consistency in the parameter estimates among some of the stocks, though not for all. Generally, the estimated probabilities of not counting a true ring are higher than the probabilities of counting two rings where there is only one. This suggests an increasing bias to under estimating the true age as fish get older. Ageing errors are likely common among the stocks, and simultaneously analyzing the data for all the stocks while estimating common ageing error parameters would be a reasonable way to investigate ageing errors.

Table 11. Estimates of ageing error (- and + are the probabilities of either not counting a ring or counting two rings, for each true ring in the structure) . Estimates are from HCAM runs R5, R11, R13 and R14 for the five herring stocks.

	R5		*R11*		*R13*		*R14*	
stock	-	+	-	+	-	+	-	+
GS	0.012	0.014	0.009	0.015	0.000	0.016	0.004	0.015
WCVI	0.021	0.014	0.015	0.012	0.020	0.014	0.000	0.015
CC	0.018	0.004	0.009	0.006	0.000	0.005	0.003	0.008
PRD	0.004	0.017	0.009	0.015	0.001	0.027	0.004	0.021
QCI	0.022	0.005	0.021	0.006	0.012	0.005	0.000	0.003

The set of runs R6 have parameterization like the R4 set except that the "plus" group is decreased from 10 to 7. This changes the data that is being fitted, so it is not appropriate to compare objective function values among runs R4 to R6. With a younger "plus" group the magnitude of the overall mean age composition residuals is reduced, but the pattern of predominantly negative residuals for the younger and oldest age-classes and positive residuals for the intermediate age-classes remains (Table 10). For 3 of the 5 stocks (WCVI, CC, and PRD), the age composition normalized residuals statistics, SDNR and MAD, are worse with the lower "plus" group (compare runs R4 and R6 in Table 9).

Neither of the options for dealing with ageing error, direct estimation of ageing errors or reducing the age of the "plus" group, provides a great improvement in the age composition residual patterns, so there is no strong basis to choose between them. We adopt a compromise, and retain the ageing error parameterization and reduce the "plus" group to age 9. Results from this compromise parameterization are shown as run R7.

Run R8

The set of runs R8 are an extension of runs R7 with the addition that age-dependent natural mortality is estimated. Age-dependent natural mortality is parameterized as a linear change in natural mortality beginning at age 4. This assumption adds one free parameter to the estimation.

The assumption of age-dependent natural mortality provides a slight improvement in the overall model fits for all stocks (Table 9) and provides a reasonable improvement in the residual patterns of the age composition data (Table 10). Thus we retain this assumption in further runs.

R9

The set of runs R9 are the same as the R8 set, except for the addition of estimating time-varying natural mortality, which is parameterized as a random walk. This increases the number of free parameters that are estimated by 55.

The time-varying natural mortality assumption produces improvements in fit primarily for the spawn index data, and to a lesser extent for the age composition data. This is seen both in decreased values of the negative log-likelihood for these data (Appendix Table 3) and in decreased values for the normalized residuals statistics, SDNR and MAR (Table 9). Also, the autocorrelation in the spawn index residuals is reduced for all stocks (Table 9).

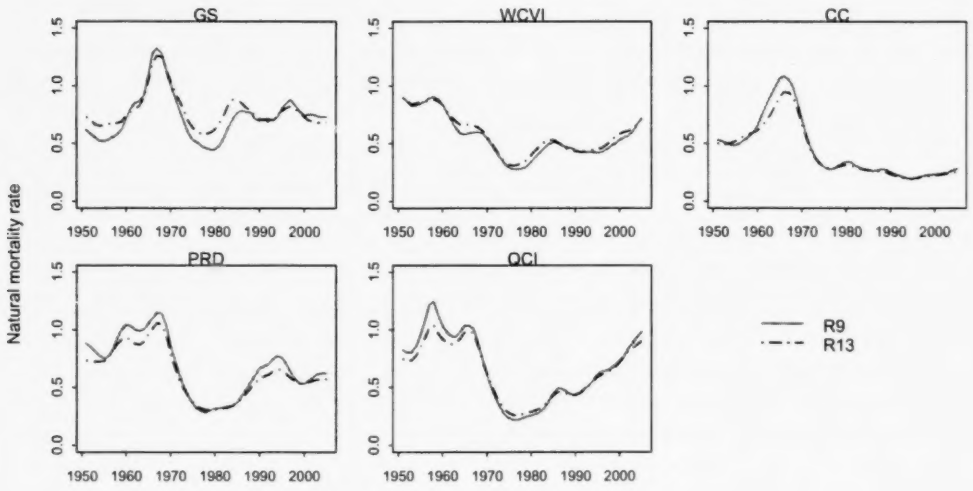

Figure 11. Natural mortality estimates for HCAM runs R9 and R13 for the five herring stocks.

The patterns in the natural mortality estimates show some similarities among the stocks, with high natural mortality rates during the 1960's decreasing to low natural mortality rates in the 1970's (Figure 11). Since then, the natural mortality rates have increased in all stocks except for CC.

The random-walk natural mortality parameterization provides major improvements in all aspects of the model fits and is retained in further runs.

R10

The R10 set of runs builds on the structure of the R9 set and estimates a second spawn index proportionality constant (q) for the period 1988-2005. The prior on this second q is uniform between 0.7 and 1. The rationale for this is that a small proportion of the spawning events are not surveyed and there is a loss of eggs between the spawning events and the surveys due to predation. While both of these effects would decrease q from 1, the prior is *ad hoc*.

Estimating a second spawn index proportionality constant improves the model fits, though for some stocks (eg. WCVI and QCI) the improvement is very small. For all stocks, the autocorrelation in the spawn index residuals decreases (Table 9).

For all stocks, the 1988-2005 spawn index qs are at their lower bound (Table 12). This is an unsatisfactory result, given that the prior on this q is *ad hoc*. We conclude that inclusion of this second spawn index proportionality parameter in the herring model is not warranted until such time that an informed prior can be developed for it. An informed prior could be developed based on studies that have investigated herring egg loss due to predation and estimates of the proportion of spawning events that are not surveyed. It is interesting to note that inclusion of the spawn q for 1988-2005 has little effect on the estimates of the spawn q for 1951-1987 (Table 12). To investigate the assumption that the spawn index q=1 for recent years introduces a negative bias to the estimates of spawning abundance, we evaluate the effect of estimating a second spawn index q on the retrospective patterns in a later section.

Table 12. Estimates of the spawn index proportionality "q's". Estimates are from HCAM runs R9, R10, and R13 for the five herring stocks. Note that for runs R9 and R13 the 1988-2005 q's are fixed at 1.

Stock	R9		R10		R13	
	1951-1987	1988-2005	1951-1987	1988-2005	1951-1987	1988-2005
GS	0.79	1.00	0.69	0.70	0.60	1.00
WCVI	0.83	1.00	0.79	0.70	0.78	1.00
CC	0.31	1.00	0.28	0.70	0.35	1.00
PRD	0.42	1.00	0.38	0.70	0.50	1.00
QCI	0.60	1.00	0.54	0.70	0.56	1.00

R11

The set of runs R11 builds on the R9 set and introduces deviations from the selectivity functions. Deviations are estimated for each fishery, so this adds between 78 and 119 additional parameters to the estimation.

Model fits are improved substantially when we allow deviations from the average selectivity functions. Many of the normalized residuals statistics, the SDNR and MAR, are now close to their expected values (Table 9). The notable exceptions are the age composition residuals for the PRD and QCI stocks, which are still larger than their expectations. Also, the age composition residuals for the GS stock are smaller than expected, suggesting this data is being under-weighted. The over-riding pattern in the age-specific residuals is improved, but there is still a preponderance of positive residuals for age-classes 7 and 8 and negative residuals for the "plus"

age-class (Table 10). Quantile plots of these residuals indicate this pattern is largely driven by a lack of fit to the GN fishery data, and to a lesser extent the SN-roe fishery data (Figure 12).

The inclusion of fishery-specific deviations from the average selectivity function decreased the magnitude of the time trends in the natural mortality estimates (Figure 11). Also, the autocorrelation in the spawn index residuals is reduced for most stocks (Table 9).

R12

The set of runs R12 is the same as the set R11 with the addition that a 1988-2005 spawn index proportionality constant is estimated. We introduce this run so that we can investigate its retrospective pattern.

R13 and R14

The selectivity deviations introduced in runs R11 substantially improved the model fit (smaller age composition and spawn index residuals), but this parameterization requires a large number of additional parameters to be estimated. Alternative approaches to dealing with the magnitude of the age composition residuals are to either use the robust-normal likelihood or to increase the process error variance in the multinomial likelihood. We evaluate both approaches and compare results with those where deviations from average selectivity are assumed.

For runs R13 we increased the age composition process error variance so that the total objective function values were similar to runs R11 (from 0.003 to 0.009). Otherwise this set of runs is the same as the R9 set. Overall the pattern of age composition residuals for this run is an improvement over run R11, with smaller average residuals for all age-classes, and in particular for age-classes 7 through 9+ (Table 10). Quantile plots of the distribution of these normalized residuals show that for the winter fishery the magnitude of the residuals tend to be larger for the younger age-classes than for the older age-classes (Figure 13). The results are equivocal as to whether it is better to estimate selectivity deviations or to allow a larger process error in the fits to the age composition data, though from the perspective of parsimony the R13 run would be preferred.

For runs R14 we use the robust-normal likelihood in fitting to age composition data (with the multinomial until the final phase). Otherwise these runs are the same as runs R9. The pattern of age composition residuals for this run are worse than those from the R11 fits, with larger positive residuals for the younger age-classes (Table 10). Overall, the age composition SDNR and MAR statistics are similar to those from the R11 fits. As for the R13 set of runs, the residuals for the younger age-classes tend to be larger than those for the older age-classes (Figure 14).

There is no strong basis for deciding whether to model selectivity deviations, to assume higher process error in the fits to age composition data, or to use the robust-normal likelihood. We did investigate alternative sequences in the phased estimation of parameters for the R11 set of runs, and did find some examples where different local minima occurred. We did not attempt similar analyses for the R13 and the R14 set of runs, but if one of these approaches were able to generate consistent minima with alternative phasing this could be a criteria for selecting the best approach.

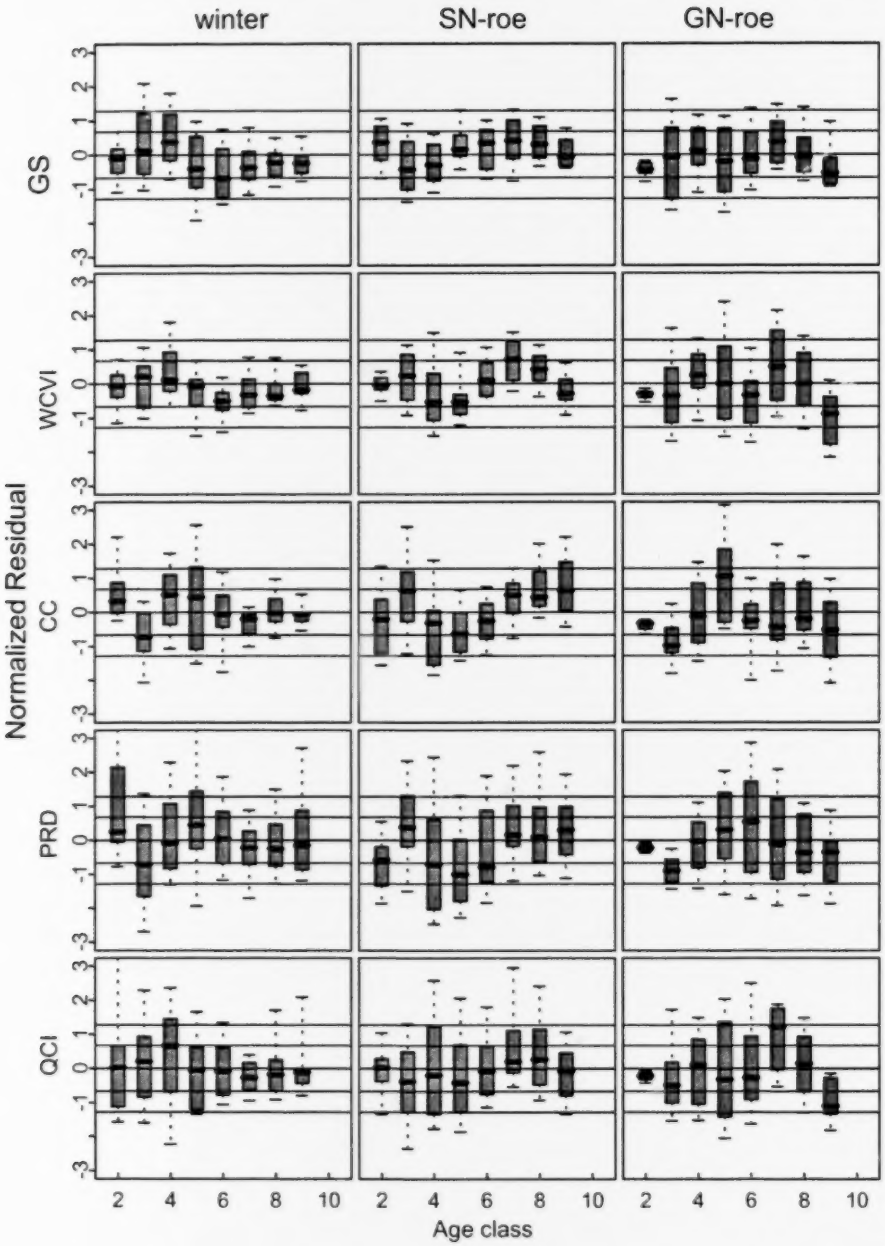

Figure 12. Quantile plots of normalized residuals from age composition fits for the R11 HCAM model, by fishery and stock. The shaded boxes show the inter-quartile range (with the median shown by the solid bar) and the whiskers show the 10th and 90th quantiles. The horizontal lines indicate the expected values for the 10th, 25th, 50th, 75th, and 90th quantiles.

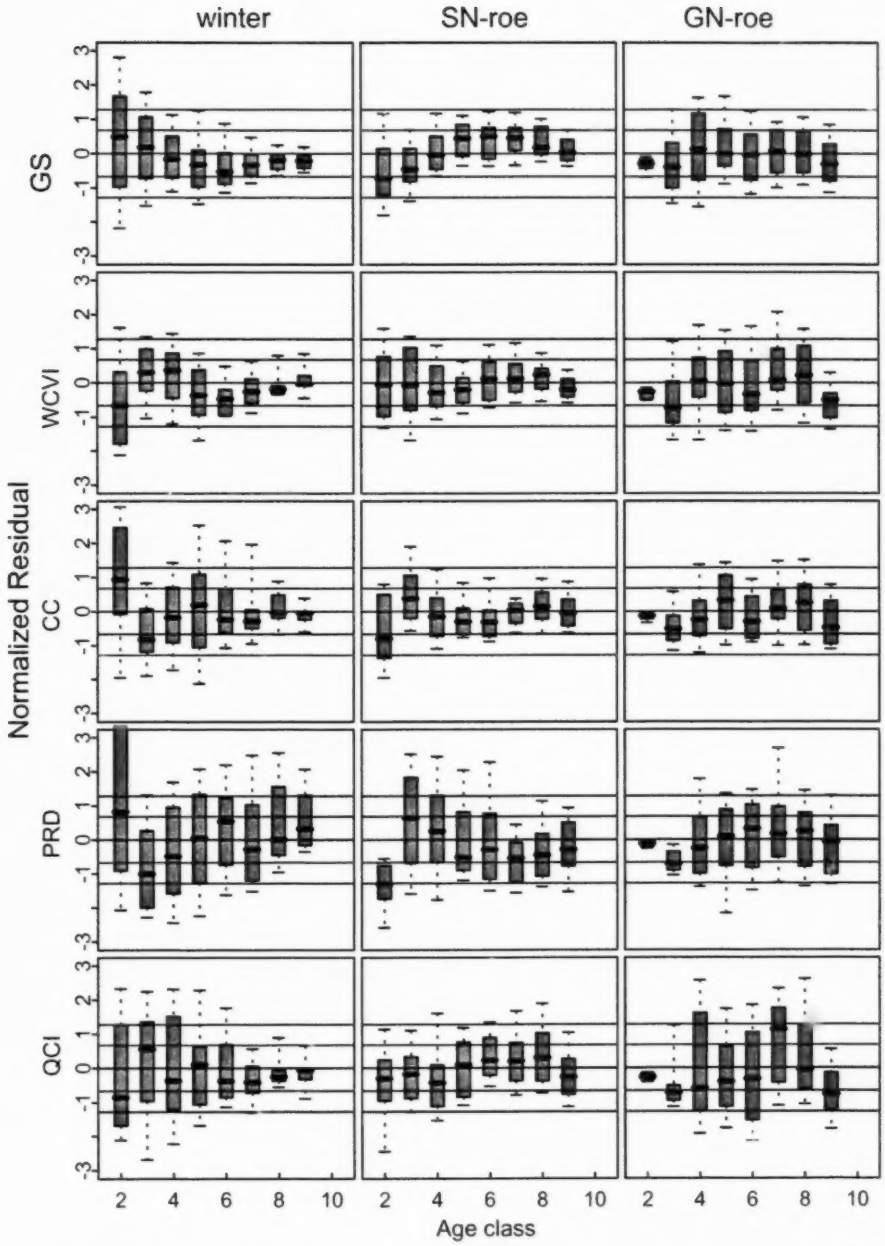

Figure 13. Quantile plots of normalized residuals from age composition fits for the R13 HCAM model, by fishery and stock. The shaded boxes show the inter-quartile range (with the median shown by the solid bar) and the whiskers show the 10th and 90th quantiles. The horizontal lines indicate the expected values for the 10th, 25th, 50th, 75th, and 90th quantiles.

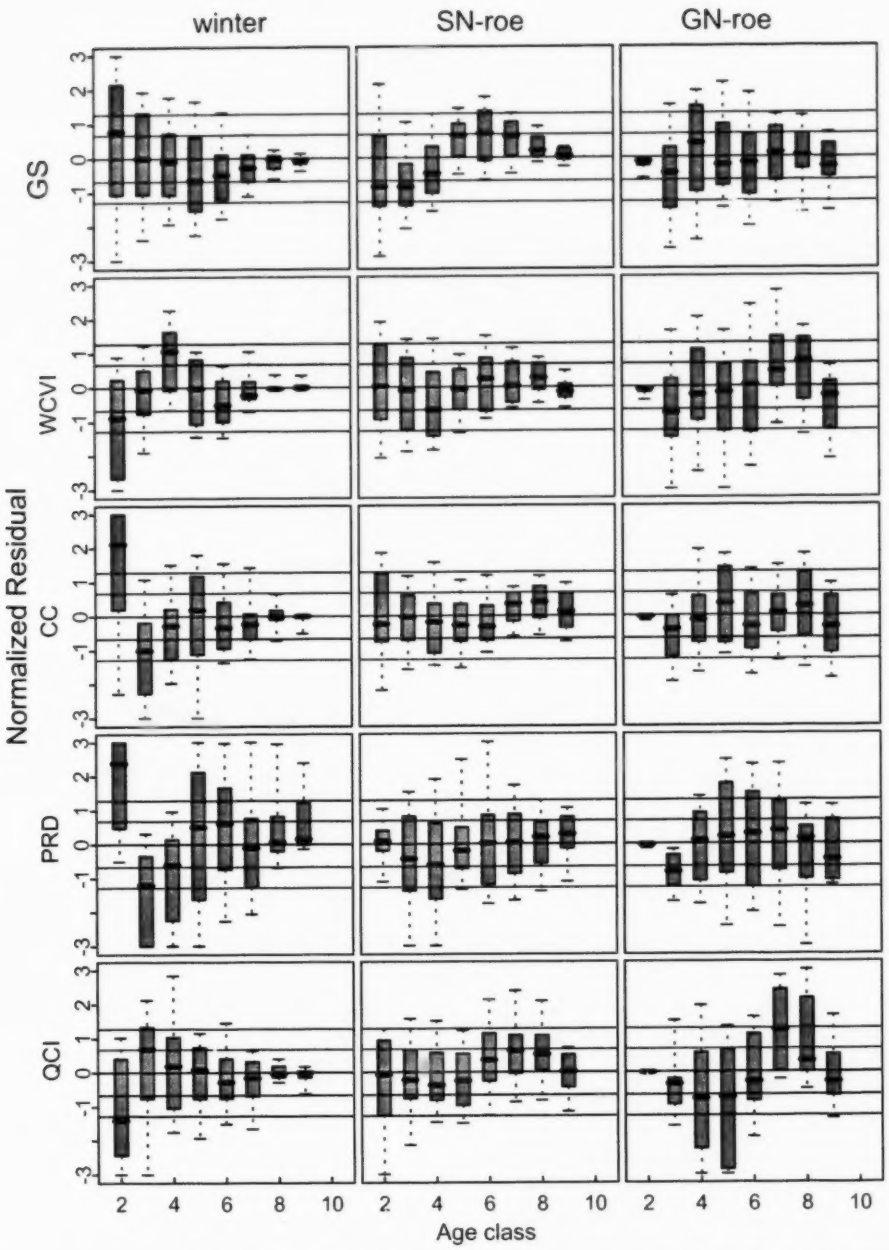

Figure 14. Quantile plots of normalized residuals from age composition fits for the R14 HCAM model, by fishery and stock. The shaded boxes show the inter-quartile range (with the median shown by the solid bar) and the whiskers show the 10th and 90th quantiles. The horizontal lines indicate the expected values for the 10th, 25th, 50th, 75th, and 90th.

Retrospective Analyses

Retrospective analyses were conducted using the HCAM model to assess whether the stock reconstructions remained stationary as additional years of data become available. Analyses were conducted fitting to the data series with terminal years from 1996 through 2003. We calculated the same statistics as for the EASM-like and NASM-like models to measure the degree to which biomass estimates change as additional years of data are added to the estimation. Retrospective analyses were done for the R9 and R11 through R14 model structures so that we could assess whether estimating the second spawn index proportionality constant, estimating selectivity deviations, or the alternate methods of dealing with age composition residuals were influential in the retrospective patterns. Results are shown in Table 13.

Table 13. Summary statistics for retrospective changes in stock biomass estimates from the HCAM model runs (R9 and R11 through R14) for the five herring stocks.

		$100\left(B_y^y - B_y^{2005}\right)/B_y^{2005}$									
Run	Stock	Mean	Mean absolute	1996	1997	1998	1999	2000	2001	2002	2003
R9	GS	27.3	27.3	29.9	5.2	30.4	34.5	43.3	37.3	23.6	14.4
	WCVI	2.7	10.4	18.5	4.2	-15.9	-3.9	-2.4	16.0	13.6	-8.4
	CC	2.4	13.3	-27.2	-15.1	8.8	19.7	6.0	-1.3	11.5	16.9
	PRD	22.3	27.0	34.6	51.5	56.3	31.5	13.4	-15.1	10.0	-3.6
	QCI	-2.7	17.1	-7.2	20.6	5.7	-15.0	-1.1	-56.0	29.4	2.0
	Mean	10.4	19.0								
R11	GS	19.4	19.9	26.1	34.1	31.5	19.2	-2.2	18.9	15.2	12.3
	WCVI	-16.9	17.7	3.0	-24.7	-32.2	-35.3	-22.8	-4.9	-5.8	-12.4
	CC	9.9	15.2	21.7	21.6	25.5	22.9	9.0	-10.6	-10.0	-0.8
	PRD	-5.5	9.9	-11.6	-31.6	0.1	-1.1	9.6	-12.0	8.0	-5.4
	QCI	0.8	21.2	16.9	26.6	-4.5	11.2	16.3	-60.4	16.9	-16.4
	Mean	1.5	16.8								
R12	GS	18.7	18.8	20.4	30.0	25.7	13.5	-0.2	21.5	22.1	16.8
	WCVI	-17.1	18.2	4.2	-24.7	-33.9	-32.9	-21.0	-4.2	-7.0	-17.4
	CC	7.6	14.3	18.2	16.8	19.1	18.5	4.7	-14.0	-13.0	10.4
	PRD	-9.6	12.2	-15.0	-26.1	-0.2	-4.3	7.3	-25.9	3.1	-15.8
	QCI	-0.4	18.0	15.4	22.1	-6.4	5.1	12.3	-51.7	15.4	-15.4
	Mean	-0.2	16.3								
R13	GS	17.1	17.1	25.3	8.4	10.3	11.0	28.5	25.1	15.5	12.5
	WCVI	-3.8	12.4	9.2	-1.6	-26.3	-21.6	-6.4	13.0	12.1	-8.9
	CC	0.7	7.0	-11.0	-1.2	14.7	15.8	0.4	-10.6	-0.5	-1.9
	PRD	14.2	18.1	18.2	29.6	36.0	17.3	10.8	-15.6	12.1	4.8
	QCI	-6.4	16.2	-4.5	19.7	-1.0	-8.4	-2.8	-70.3	19.4	-3.4
	Mean	4.3	14.1								
R14	GS	25.8	25.8	34.0	15.1	19.7	22.0	34.1	31.8	34.2	15.4
	WCVI	-3.0	12.5	11.5	-2.4	-20.5	-21.4	-10.6	13.5	12.9	-7.3
	CC	2.8	12.5	-25.4	-12.3	15.6	25.9	8.9	3.2	7.8	-1.0
	PRD	15.4	20.6	15.7	32.0	34.5	14.3	7.8	-20.8	22.4	17.4
	QCI	-7.4	16.8	-7.7	23.3	1.3	-10.9	-5.7	-69.6	13.1	-2.8
	Mean	6.7	17.6								

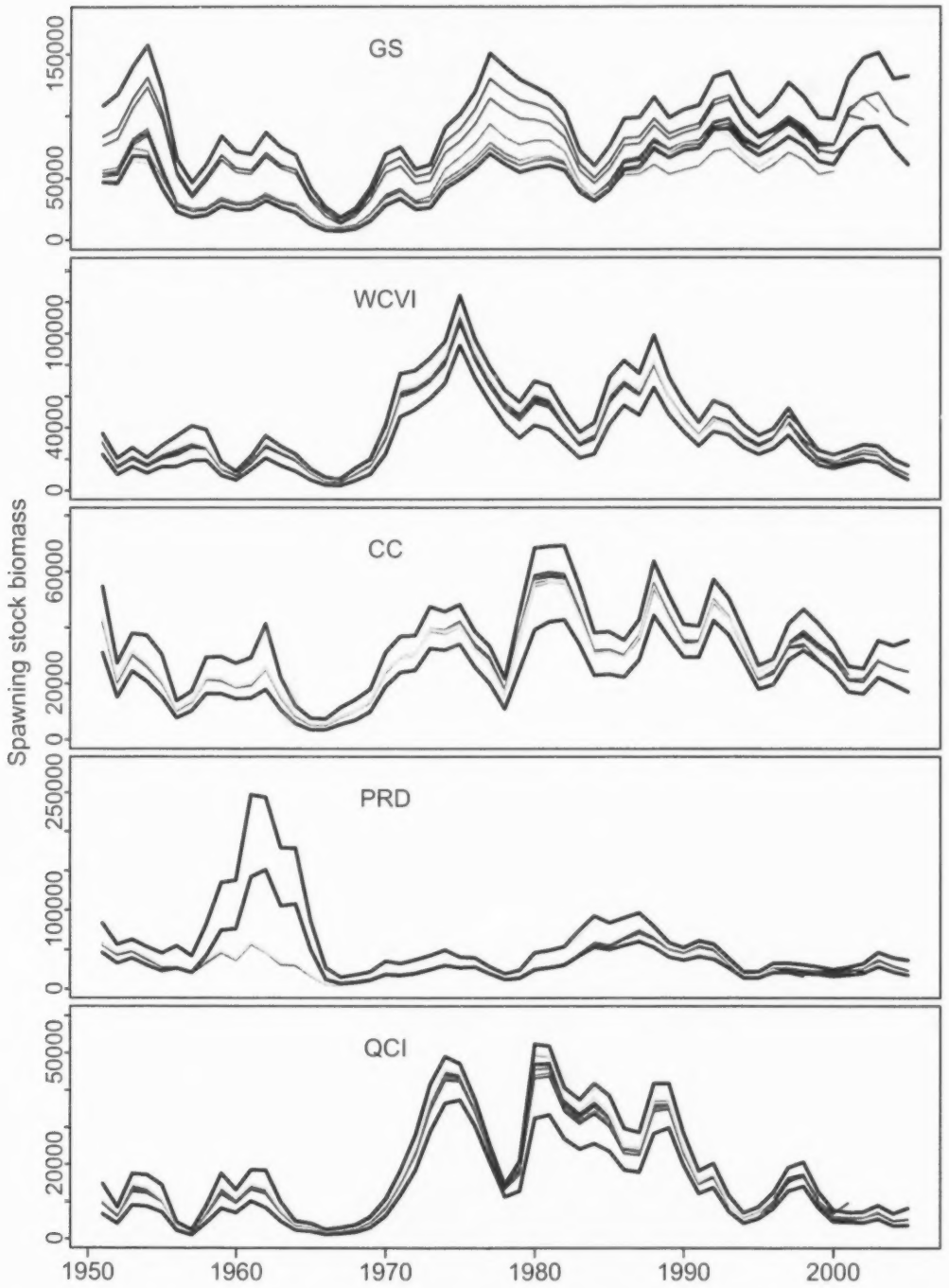

Figure 15. Estimates of spawning stock biomass from retrospective analyses (1996-2003, light coloured lines) and from marginal posterior estimates (using data through 2005, 10th and 90th percentiles of the distribution are shown as heavy lines). Results are from analyses using the R13 model parameterization.

Overall there tends to be a small positive bias between the initial estimates of spawning abundance and those from the 2005 assessment, with the R9 run having the largest bias. None of the model formulations resulted in consistently better retrospective patterns across all stocks, though R13 had the lowest mean absolute residuals for three of the five stocks. Inclusion of a second spawn index proportionality constant (R12) did not improve the retrospective pattern, and exclusion of the selectivity deviation parameters (R9) resulted in slightly poorer retrospective patterns. Overall, the R13 model formulation had the lowest mean absolute error with an average 14.1 percent error (Table 13). The retrospective patterns are smaller for the HCAM series of runs than for either the EASM or HASM-like model formulations.

For the set of R13 runs we estimated the joint posterior distribution using the ADMB MCMC algorithm. The marginal posterior distributions of spawning stock biomass (the 10^{th} and 90^{th} percentiles) are shown in Figure 15 along with the retrospective spawning stock biomass estimates for R13. In general, the retrospective abundance trends are within the 10^{th} and 90^{th} percentiles of the marginal posterior distributions from the analysis using the full (through 2005) data set.

Other diagnostics were also examined for the run R13 MCMC chains and the marginal posterior distributions of some parameters. In general the MCMC chains did not show any problems with non-convergence, though for the GS stock a longer chain would have been useful to ensure convergence. Comparison of marginal posterior distributions with their priors show that the stock-recruitment variance parameter, sigmaR, is fairly well determined with posterior distributions at the upper end of the priors for all stocks except for GS (Figure 16). The stock recruitment steepness parameter also appears to be reasonably well determined, with little posterior density at the lower steepness values (Figure 17).

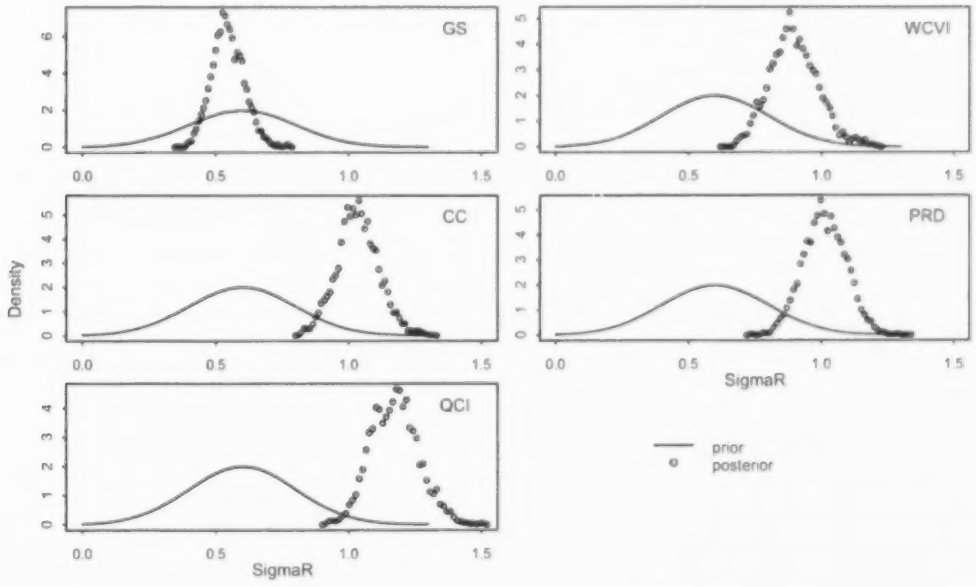

Figure 16. Marginal posterior and prior distributions for the stock-recruitment variance parameter (SigmaR) from runs R13 for the 5 herring stocks.

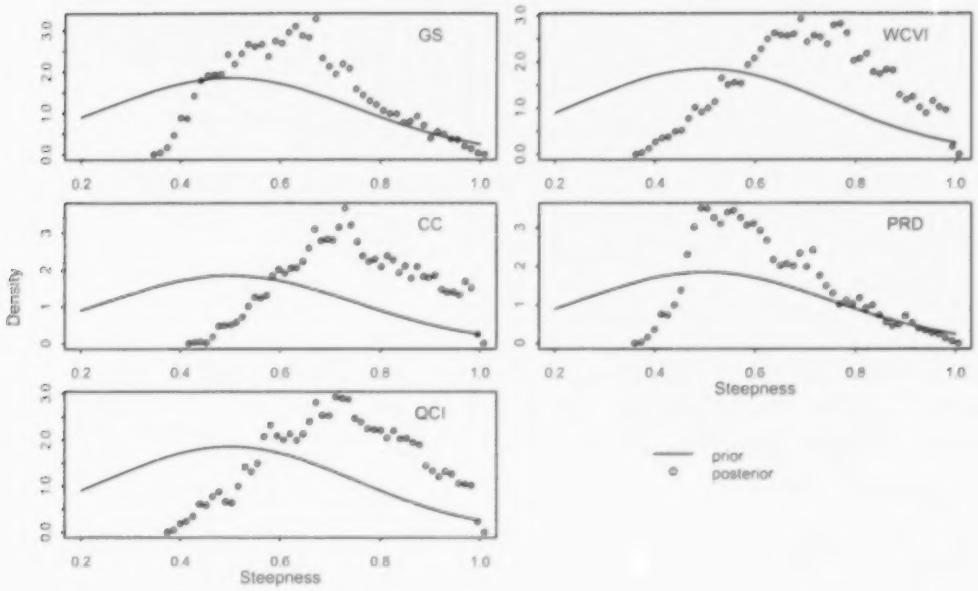

Figure 17. Prior and marginal posterior distributions for the stock-recruitment steepness parameter from runs R13 for the 5 herring stocks.

COMPARISON OF EASM AND HCAM-R13 STATISTICS OF MANAGEMENT CONCERN

We compared some model output quantities that impact management decisions to see how the HCAM R13 results differ from those of the current stock assessment model (EASM).

Estimates of spawning stock biomass from the EASM and the HCAM R13 runs, based on the full data series (i.e. data through 2005), are shown in Figure 18. The general patterns in spawning abundance are similar for the two models though there are some significant differences between the absolute magnitude of spawning abundance for some of the stocks. In particular, for the GS and CC stocks the HCAM R13 model consistently estimates higher spawning abundance than the EASM. For the other stocks, differences tend to be minor or occur only over time intervals.

For each year of the retrospective analyses stock projections were made to compare TAC expectations from the EASM and the HCAM R13 model formulations. The stock projections assumed recruitment of 3-year olds would be equal to the average over the historic period, a full years' mortality would occur prior to the fishery, and a 20% harvest rate. For the EASM runs the results are from the MLE estimates, which is consistent with the process currently used. For the HCAM R13 runs results are from the MPD estimates for all years of the retrospective analysis. For the 2005 analyses we had also completed the full Bayesian estimation, so for that year we also present results based on the median of the projected stock biomass' over the MCMC chain

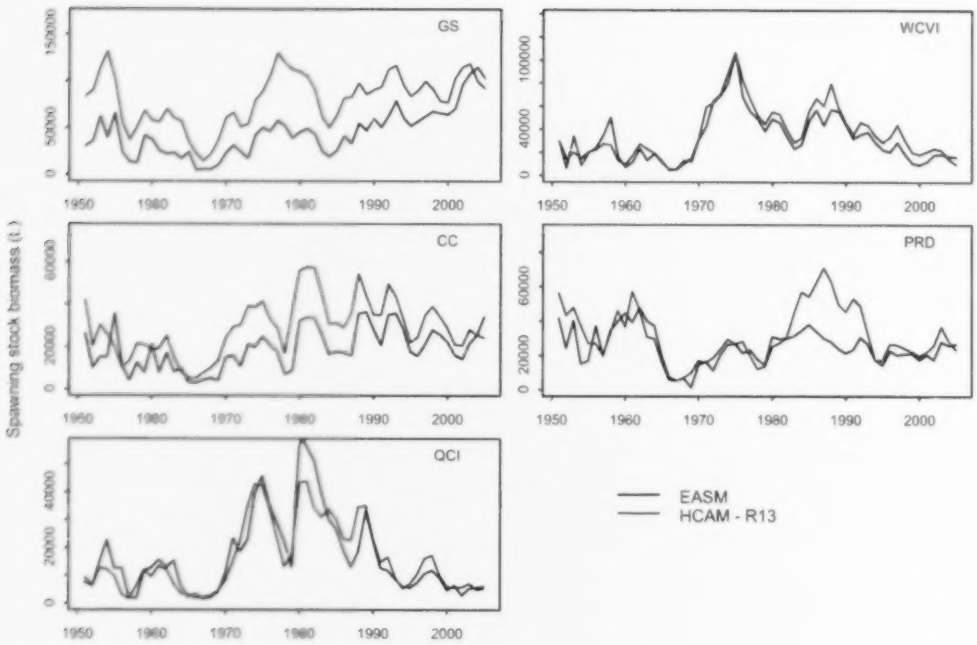

Figure 18. Estimates of spawning stock biomass from the EASM and from the HCAM R13 model formulation for the 5 herring stocks.

for comparison. The differences between the EASM and HCAM R13 projected TAC's are shown in Table 14.

TAC projections are consistently lower for the HCAM R13 model formulation than for the EASM formulation for all stocks except for CC. This result appears to be due to the EASM retrospective bias whereby additional years' data tend to decrease earlier stock estimates from this model. The differences between the EASM and HCAM projections are less when the median of the HCAM posterior distribution of projected biomass is used for the projections than when the MPD of projected biomass is used for the projections (compare 2005 MCMC and MPD differences in Table 14). Full Bayesian analyses were not conducted for each of the retrospective years, so it is not possible to evaluate how different these would be to the MPD estimates. For Bayesian estimation the appropriate statistics to use are from the posterior distribution rather than the MPD estimates.

Table 14. The difference between EASM and HCAM R13 TAC projections (20% of projected biomass in tonnes) for the retrospective runs from 1996 through 2005. EASM projections are all based on the MLE, while HCAM projections are primarily from the MPD estimates. For the 2005 analysis the median from the MCMC analysis are presented for comparison with the MPD results.

Method	Year	GS	WCVI	CC	PRD	QCI	All stocks
MCMC	2005	-3057	-2857	-1631	1986	-983	-6542
MPD	2005	-1519	-3089	-1936	-972	-1091	-8607
MPD	2003	-4009	-2486	292	-1167	-2528	-9898
MPD	2002	-1863	-2967	167	-131	-1145	-5938
MPD	2001	-4081	-1676	863	-311	-1398	-6602
MPD	2000	-5936	-662	792	-497	-575	-6879
MPD	1999	-4360	-163	680	-469	-968	-5280
MPD	1998	-2915	-361	565	-2219	-3565	-8495
MPD	1997	-2506	-186	2179	-1460	-1479	-3451
MPD	1996	-5498	-233	2530	-2000	-644	-5846

SUMMARY AND CONCLUSIONS

The primary areas of concern we found in the EASM-like and NASM-like model analyses was that the data were over-weighted (that is, residuals tended to be over-dispersed relative to the error assumed for individual data components) and there was a strong age-related pattern in the residuals from the fits to the age composition data. Given the larger number of parameters in these models, one would hope for more balanced residuals.

An implementation of the HCAM was developed for analyzing the herring fisheries data that we believe has better performance than either the EASM or the NASM, although it incorporates aspects of both the EASM and the NASM. Diagnostics from the HCAM implementation that we believe indicate better performance are: a reduction in the magnitude of the retrospective pattern; a reduction in the magnitude of the age-related pattern in age composition residuals, and better coherence between the assumed and empirical estimates of the lack of model fit to the data.

HCAM is structured for Bayesian estimation, which we believe is superior to maximum likelihood estimation for fisheries assessment models because it facilitates estimation of the uncertainties in estimated and derived parameters. Additionally, a Bayesian approach facilitates estimation of parameters for which there is generally little information in the data through the influence of the priors. An example is the stock-recruitment parameter *steepness*, which is generally not well determined from fisheries data. However, results from meta-analyses can provide informed priors (estimated for species groups) for this parameter (Myers et al. 2002) improving the consistency of its estimation.

Bayesian estimation performs best with well-developed informed priors. For these analyses, we did not attempt to develop informed priors, but rather adopted those specified for the NASM analysis or specified *ad hoc* priors. Additional work to develop informed priors would benefit the herring assessments. These could be based on additional data and information not directly used in the assessment or based on published results from meta-analyses. In particular, the priors

on the spawn index proportionality constants "q" should be informed priors, and there is additional data not used in the model from which the priors could be developed.

The NASM analysis models annual variation in natural morality rates as independent annual events, whereas the HCAM analyses assume trends in the annual changes in natural mortality rates (i.e. a "random walk"). The rationale for the NASM parameterization of natural mortality is to allow for episodic emigration events (Ware and Schweigert, 2001) as well as inter-annual variation in predation rates. We prefer the "random walk" parameterization because emigration or immigration events should be estimated by modelling the herring populations simultaneously to ensure the emigration and immigration events balance and changes in predation rates are likely to change slowly over time rather than with annual random variation. We did not explore other alternative assumptions regarding annual changes in natural mortality, for example Haist et al. (1993) found evidence for density dependent natural mortality rates in the B.C. herring stocks.

Alternative methods for improving model fits to the age composition data sets and reducing the impact of large outliers were examined. These included; assuming fishery-specific deviations from the age-specific average selectivity, assuming a larger variance for the process error in fits to the age composition data, and using a robust-normal likelihood which down-weights large residuals in fitting the age composition data. None of these approaches were clearly superior, though the assumption of fishery-specific deviations from the average selectivity resulted in residuals that were more evenly distributed across age classes.

Evidence that local minima solutions were often obtained when fitting to the herring data sets was found for both the NASM-like and HCAM R11 model structures. No such evidence was found for the EASM-like model, and other HCAM runs were not examined for possible local minima estimates. Further work evaluating alternative phase sequences for adding model parameters to the estimation, may show a phase sequence that can consistently provide the best fits to the data.

Aspects of the HCAM parameterization that were not examined in these analyses include; the stock-recruitment function, alternative approaches to initializing the populations, and using the instantaneous form of the catch equations. Additional work to evaluate these options is warranted.

ACKNOWLEGEMENTS

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Appendix A. Description of the generic herring catch-age model (HCAM).

The herring catch-age model partitions the populations by region, year, fishing period, sex, and age. Because the analyses presented in this document do not use the region and sex partitions and for ease of presentation, this description does not include notation for those options.

The following table describe model parameters:

Parameter	Description
Derived parameters	
$N_{i,j}$	The number of fish of age j at the beginning of year i
$N'_{i,p,j}$	The number of fish of age j at the beginning of period p of year i that are available to the fishery
B_i	The spawning stock biomass in year i
$F_{i,p,j}$	The instantaneous fishing mortality for fish of age j during fishing period p and year i
$M_{i,p,j}$	The instantaneous natural mortality for fish of age j during fishing period p and year i
$M_{i,\bullet,j}$	The total natural mortality for fish of age j during year i
R_i	The recruitment in year i
$\lambda_{i,j}$	Proportion of fish at age j available to the fisheries in year i
$s_{i,p,j}$	Selectivity at age j for fishing period p in year i
α, β	Parameters of the stock-recruitment relationship
$\hat{C}_{i,p,j}$	Fitted catch at age j (numbers) during fishing period p and year i
$\hat{p}_{i,p,j}$	Fitted proportion at age j during fishing period p and year i
Indices	
i, i_1, i_h	Indexes year: i_1 and i_h are the first and last years, respectively
j, j_1, j_h	Indexes age-class: j_1 and j_h are the first and last age-classes, respectively
p, p_h	Indexes fishing period: p_h is the final fishing period
a_1	First age-class with age-dependent natural mortality trend
Observations	
$\tilde{C}_{i,p}$	Catch in mass or numbers during fishing period p and year i
$\tilde{p}_{i,p,j}$	The proportion of fish at age j in the catch of fishing period p and year i
$\tilde{S}_{i,p}$	The number of fish aged for fishing period p and year i
$\tilde{I}_i$	Spawn index in year i
$w^S_{i,j}$	Mean spawning weight of fish at age j in year i
$w^C_{i,j}$	Mean weight of fish in the catch at age j in year i
$w^G_{i,j}$	Geometric mean weight of fish at age j in year i in the gillnet catch

The following table describes parameters that are estimated through the minimization:

Parameter	Description
R_0	Average recruitment (at unfished equilibrium, when S-R assumed)
d_i^R	Recruitment deviations
h	Stock-recruitment steepness
ψ_1	Average natural mortality rate
ψ_2	Age-dependent mortality parameter
d_i^M	Annual deviations for natural mortality
σ_R^2	Variance of recruitment
$\gamma_{p,k}$	Selectivity ogive parameters for fishery p
$d_{i,p}^S$	Fishery-specific selectivity deviations
v_k	Availability ogive parameters
d_i^A	Annual deviations from average availability
η_j	Parameters for the number of fish of age j in the first year
$F''_{i,p}$	Fully-selected fishing mortality rates for fishery p in year i
q_1, q_2	Spawn index proportionality constants for periods 1 and 2
a^-, a^+	Probabilities for not counting an age ring and counting two rings where only one is present

The model description follows.

Fishing and population dynamics:

The following equations describe the population and fishing dynamics:

$$N'_{i,1,j} = \lambda_{i,j} N_{i,j} \qquad j_l \le j \le j_h$$

$$N'_{i,p+1,j} = \exp\left(-M_{i,p,j} - F_{i,p,j}\right) N'_{i,p,j} \qquad 1 \le p \le p_h$$

$$N_{i+1,j+1} = N'_{i,p_h+1,j} + \left(1-\lambda_{i,j}\right)\exp\left(-M_{i,\bullet,j}\right) N_{i,j} \qquad j_l \le j < \left(j_h - 1\right)$$

$$N_{i+1,j+1} = N'_{i,p_h+1,j} + \left(1-\lambda_{i,j}\right)\exp\left(-M_{i,\bullet,j}\right) N_{i,j} + N'_{i,p_h+1,j_h} + \left(1-\lambda_{i,j_h}\right)\exp\left(-M_{i,\bullet,j_h}\right) N_{i,j_h} \qquad j = j_h - 1$$

$$N_{i,j_l} = R_i$$

$$B_i = \sum_j w_{i,j}^S m_j N'_{i,p_h+1,j}$$

For the NASM-like implementation of the model the, λ_{ij} parameters are fixed at 1.

For the EASM-like implementation, which assumes that the available fish represent the mature component of the population, the maturity parameters m_j are set to 1.

Catch equations:

There are two options for describing how catch is taken, the instantaneous (Baranov) catch equations and the discrete catch equations.

The form of the instantaneous (Baranov) fishing mortality equation is:

$$\hat{C}_{i,p,j} = \frac{F_{i,p,j}}{F_{i,p,j} + M_{i,p,j}} \left(1 - \exp(-F_{i,p,j} - M_{i,p,j})\right) N'_{i,p,j}$$

where $F_{i,p,j} = s_{i,p,j} F''_{i,p}$. The fully selected fishing mortality rates, $F''_{i,p}$, can be calculated iteratively through a Newton-Raphson algorithm or estimated as free parameters (as is done in EASM).

The form of the discrete catch equation is:

$$\hat{C}_{i,p,j} = \exp\left(-M_{i,p,j}\right) s_{i,p,j} F'_{i,p} N'_{i,p,j}$$

where there are two options for estimating the $F'_{i,p}$: 1) as free (estimated) model parameters, or 2) $F'_{i,p} = \tilde{C}_{i,p} \Big/ \sum_j \left(\exp\left(-M_{i,p,j}\right) s_{i,p,j} w^C_{i,j} N'_{i,p,j}\right)$. Note that first option assumes errors in the total catch data and the second option assumes no errors in the total catch data. For the discrete catch equations the variables $F_{i,p,j}$ are estimated as: $F_{i,p,j} = -\ln\left(s_{i,p,j} F'_{i,p}\right)$.

When the catch data is in numbers the average fish weight $w^C_{i,j}$ is set to 1. The discrete form of the catch equations is used in the NASM-like model and the HCAM model runs.

Parameterizing age-dependent availability and selectivity:

Age-dependent selectivity can be parameterized using the following functions:

Logistic NASM: $$s_{i,p,j} = \left(1 + \exp\left(-\gamma_{p,2}\left(j - \gamma_{p,1} \exp\left(d^S_{i,p}\right)\right)\right)\right)^{-1}$$

Logistic EASM: $$s_{i,p,j} = \left(1 + \exp\left(\frac{-\ln(19)}{\gamma_{p,2}}\left(j - \gamma_{p,1} + d^S_{i,p}\right)\right)\right)^{-1}$$

Logistic EASM GN: $$s_{i,p,j} = \left(1 + \exp\left(-\gamma_{p,2}\left(w^g_{i,j} - \gamma_{p,1} \exp\left(d^S_{i,p}\right)\right)\right)\right)^{-1}$$

Free-Age: $$s'_{i,p,j} \begin{cases} 0 & j < l_l \\ \gamma_{p,j} & l_l \le j \le l_h \\ 1 & j > l_h \end{cases}$$

For this parameterization, deviations are applied using odds-ratios to ensure the resultant parameter values remain between 0 and 1:

$$s''_{i,p,j} = \left(\exp\left(d^S_{i,p}\right) s'_{i,p,j}\right) \Big/ \left(1 - s'_{i,p,j}\right)$$

$$s_{i,p,j} = s''_{i,p,j} \Big/ \left(1 + s''_{i,p,j}\right)$$

When fishery-dependent deviations are not estimated (i.e. $d^S_{i,p}$=0) then $s_{i,p,j} = s'_{i,p,j}$.
The set of functions that can be used to define selectivity can also be used to define age-dependent availability. In that case the variables $s_{i,p,j}$ are replace by $\lambda_{i,j}$ and the free parameters $\gamma_{p,k}$ and $d^S_{i,p}$ are replaced by ν_k and d^A_i.

Natural Mortality:

Natural mortality is apportioned across the fishing periods based on user specified mortality fractions $\left(f_p\right)$ for each period:

$$M_{i,p,j} = f_p M_{i,\bullet,j} \qquad \text{where } 0 \le f_p \le 1 \text{ and } \sum_p f_p = 1$$

As with fishing mortality, there are a number of options coded in HCAM for the parameterization of natural mortality. The annual instantaneous natural mortality rates can vary annually, either with a time-series component or not. Also, they can be age-dependant.

M estimated as free parameter:

$$M_{i,\bullet,j} = \psi_1 .$$

The parameterization of annual deviations:

$$M_{i,\bullet,j} = \bar{M} \exp\left(d^M_i\right) \qquad \text{where } \bar{M} = \sum_i \sum_j M_{i,\bullet,j} \Big/ n$$

where *n* is the product of the number of years and the number of age-classes in the model. Note that the above equations require a recursive solution. This form is based on the NASM parameterization and is only sensible in the Bayesian context.

The parameterization of annual deviations as a random walk is:

$$M_{i_1,\bullet,j} = \psi_1$$
$$M_{i,\bullet,j} = \exp\left(d^M_i\right) M_{i-1,\bullet,j} \qquad i_1 > i \le i_k$$

The parameterization of age-dependent M is:

$$M_{t,\bullet,j} = M_{t,\bullet,j-1} + (j - a_l + 1)\psi_2 \qquad a_l < j \le j_h$$

In the HCAM structure it is possible to model both age-dependent natural mortality and the "random walk" annual changes in natural mortality but not the combination of age-dependent natural mortality and annual deviations in natural mortality.

Stock-recruitment relationship:

A Beverton-Holt stock recruitment relationship is coded in HCAM, using the steepness parameterization of Mace and Doonan (1988):

$$R_{t+j_l} = \frac{\alpha B_t}{\beta + B_t}\exp\left(d_t^R - 0.5\sigma_R^2\right),$$

where α and β are defined in terms of B_0 and the "free" parameters h and R_0

$$\alpha = R_0\frac{(4h)}{(5h-1)} \quad \text{and} \quad \beta = B_0\frac{(1-h)}{(5h-1)}$$

and B_0, the average biomass in the absence of fishing is then given by:

$$B_0 = R_0\left(\sum_{j=j_l}^{j<j_h}\left(\lambda_{i_l,j}w_{i_l,j}^S m_j \exp\left(-\sum_{k=j_l}^{k<j} M_{i_l,\bullet,k}\right)\right) + \lambda_{i_l,j_h}w_{i_l,j_h}^S m_{j_h}\exp\left(\sum_{k=j_l}^{k=j_h} -M_{i_l,\bullet,k}\right)\left(1-\exp\left(-M_{i_l,\bullet,j_h}\right)\right)^{-1}\right)$$

This implementation of the Beverton-Holt stock recruitment relationship differs from the NASM implementation (Schweigert et al. 2006). Their parameterization includes a second average recruitment term, $\overline{R}$, in the stock-recruitment likelihood, and estimates the autocorrelation in stock-recruitment residuals.

Population Initialization:

The populations can be initialized either by assuming equilibrium conditions or by estimating the initial population with "free" parameters.

Initialization with free parameters:

$$N_{i_l,j} = \eta_j .$$

Initialization assuming equilibrium conditions:

$$N_{i_l,j} = R_0\exp\left(-Z'_j\right)$$

where $Z_j = \sum_{k=j_l+1}^{k=j} M_{i_l,k-1}$ under the assumption of no fishing prior to the first year of the analysis, and $Z_j = \sum_{k=j_l+1}^{k=j} \left(M_{i_l,k-1} + \kappa\right)$ under the assumption of a constant level of fishing (κ) prior to the first year of the analysis.

Ageing Errors:

Two options are coded in HCAM for estimating ageing errors.

Age-dependent ageing errors:

This option involves estimating a vector that defines the age-dependent probabilities of under-ageing a fish by one year $\left(a_j^-,\ \text{for}\ (j_l+1) < j \le j_h\right)$ and a second vector that defines the age-dependent probabilities of over-ageing a fish by one year $\left(a_j^+,\ \text{for}\ j_l < j < j_h\right)$. This parameterization assumes the first age-class is aged without error. An ageing error matrix (X) is constructed from these vectors. For example, given a true fish age of k, a_k^- fish will be aged k-1, $1-a_k^- - a_k^+$ will be aged k, and q_k^+ will be aged k+1.

Ring-dependent ageing errors:

The second ageing error option is based on a model developed by Francis (2003). The basic assumption is that for each ring in the ageing structure there is a probability that the ring will not be counted and second probability that two rings will be counted. Thus, the probability of ageing error increases with age and may be asymmetrical. This option involves estimating two parameters, a^-, the probability that a ring will not be counted, and a^+, the probability that for a true ring, two rings will be counted. In implementing this option we assume that the first ring is always corrected counted. The ageing error matrix (X) is built using combinatorics, treating the probability of detecting each true ring as IID events.

Spawn index proportionality constants:

Spawn index proportionality constants are defined for two periods, 1951–1987, and 1988–2005 $(q_1$ and q_2, respectively$)$. Both indices can either be fixed or estimated.

For the EASM-like and NASM-like models only the first parameter, q_1, is estimated and q_2 is fixed at 1. For the HCAM model runs, q_1 is always estimated and q_2 is estimated in a few runs (otherwise fixed at 1).

Likelihoods:

Age composition data:

The multinomial and two forms of robust-normal likelihoods are coded for fitting to age composition data. The fitted proportions at age are modified by the ageing error matrix. Let $p'_{i,p}$ be the age vector of proportions at age j before ageing error, then the fitted proportions at age after ageing error $\left(\hat{p}_{i,p}\right)$ is given by:

$$\hat{p}_{i,p} = p'_{i,p}\mathrm{X} \quad \text{where} \quad p'_{i,p,j} = \hat{C}_{i,p,j} \Big/ \sum_{j} \hat{C}_{i,p,j}$$

The negative log likelihood given the multinomial error assumption is:

$$-\log(L) = S'_{i,p} \ln\left(\hat{p}_{i,p,j}\right) - S'_{i,p} \ln\left(\tilde{p}_{i,p,j}\right).$$

Note that the second term of this equation is a constant.

The first robust-normal likelihood option was proposed by Fournier et al. (1990) to reduce the effect of outliers when fitting to proportion at length data. This likelihood is based on a multinomial-like variance for the proportions, and adds a constant term to the normal likelihood to reduce the effect of large outliers. The negative log likelihood for the Fournier robust-normal distribution is:

$$-\log(L) = 0.5\sum_{i,p,j} \ln\left(r_{i,p,j}\right) - \sum_{i,p,j} \log\left(\exp\left(\frac{-\left(\tilde{p}_{i,p,j} - \hat{p}_{i,p,j}\right)^2}{2r_{i,p,j} \Big/ S'_{i,p}}\right) + 0.01\right)$$

where $r_{i,p,j} = \left(1 - \hat{p}_{i,p,j}\right)\hat{p}_{i,p,j} + 0.01 \Big/ \left(j_h - j_l + 1\right)$.

An alternative to the robust-normal likelihood was proposed by Starr et al. (1999). They conducted simulation experiments and showed that the Fournier robust-normal could result in biased estimation. This likelihood, sometimes called the Coleraine likelihood (Bull et al. 2003), replaces the $r_{i,p,j}$ of the Fournier version with $r_{i,p,j} = \left(1 - \tilde{p}_{i,p,j}\right)\tilde{p}_{i,p,j} + 0.01 \Big/ \left(j_h - j_l + 1\right)$.

For fitting the EASM-like and HCAM model formulations we assume the "Coleraine" version of the robust normal rather than the Fournier version.

We include the option of allowing process error in the fits to the age composition data. For both the multinomial and the robust-normal likelihoods, the overall variance of a data set is proportional to its sample size. When process error is assumed, the quantities $S'_{i,p}$ are given by:

$$S'_{i,p} = \frac{1}{1/\tilde{S}_{i,p} + 1/S_{process_error}}$$

When no process error is assumed, $S'_{i,p} = \tilde{S}_{i,p}$.

Spawn index data:

Lognormal distributions are assumed for the spawn index data. The negative log likelihood is given by (ignoring the constant):

$$-\ln(L) = \frac{\sum_i \ln\left(\tilde{I}_i / q_i B_i\right)^2}{2\sigma_i^2}$$

Catch data:

For the EASM-like model, lognormal distributions are assumed for the catch data. For other implementations of the HCAM model the catch data is fitted without error. The negative log likelihood for the catch data is given by (ignoring constants):

$$-\ln(L) = \frac{\sum_i \ln\left(\tilde{C}_{i,p} / \hat{C}_{i,p}\right)^2}{2\sigma_C^2}$$

Priors:

The NASM and HCAM models are implemented for Bayesian estimation and thus require specification of priors for all "free" model parameters. These priors contribute to the objective function in the Bayesian integration.

Recruitment residuals $\left(d_i^R\right)$*:*

Stock-recruitment residuals are assumed normally distributed with mean 0 and variance σ_R^2. The prior contribution to the objective function is:

$$(i_h - i_l)\ln(\sigma_R) + \sum_{i=il+1}^{i_h}\left(\frac{\left(d_i^R\right)^2}{2\sigma_R^2}\right).$$

Stock-recruitment steepness (h)*:*

The stock-recruitment steepness parameter is assumed normally distributed with mean 0.5 and variance σ_h^2. Additionally, the steepness parameter is bounded on the interval 0.2-1.0, making this an improper prior. The prior contribution to the objective function is (ignoring the constant):

$$\frac{(h-0.5)}{2\sigma_h^2}.$$

NASM assumes a beta distribution for the steepness prior, but with the same expected value as here, so this implementation should be similar to theirs.

Stock-recruitment residual variance $\left(\sigma_R^2\right)$:

The stock-recruitment variance parameter is assumed normally distributed with mean 0.6 and variance σ_{S-R}^2. The prior contribution to the objective function is (ignoring the constant):

$$\frac{(\sigma_R-0.6)}{2\sigma_{S-R}^2}.$$

Natural mortality deviations $\left(d_i^M\right)$:

The parameters representing natural mortality deviations are assumed normally distributed with mean 0 and variance σ_M^2. The prior contribution to the objective function is (ignoring the constant):

$$\frac{\left(d_i^M\right)}{2\sigma_M^2}.$$

Selectivity deviations $\left(d_i^S\right)$:

The parameters representing selectivity deviations are assumed normally distributed with mean 0 and variance σ_S^2. The prior contribution to the objective function is (ignoring the constant):

$$\frac{\left(d_i^S\right)}{2\sigma_S^2}.$$

Availability deviations $\left(d_i^A\right)$:

The parameters representing selectivity deviations are assumed normally distributed with mean 0 and variance σ_S^2. The prior contribution to the objective function is (ignoring the constant):

$$\frac{\left(d_i^A\right)}{2\sigma_A^2}.$$

Average natural mortality rate:

The mean natural mortality rate, $\left(\bar{M} = \sum_{i,j} M_{i \bullet, j} \Big/ \left((i_h - i_l + 1)(j_h - j_l + 1) \right) \right)$, is assumed normally distributed with mean 0.45 and variance $\sigma_{\bar{M}}^2$. The prior contribution to the objective function is (ignoring the constant):

$$\frac{\left(\bar{M} - 0.45\right)}{2\sigma_{\bar{M}}^2}.$$

When natural mortality deviations are not estimated, the above equation for the mean natural mortality rate is simply, $\bar{M} = \psi_1$

Remaining parameters:

The remaining "free" parameters, R_o, $\gamma_{p,k}$, υ_k, q_1, q_2, ψ_2, a^-, a^+, are assumed to be uniformly distributed, so the prior contribution to the objective function is constant. The range of some of these uniform distributions is sometimes restricted, eg. $q_2 \sim U[0.7,1.0]$.

Residuals:

HCAM calculates two kinds of residuals, Pearson residuals and normalized residuals. Pearson residuals express the residual relative to the variability of the observation, and normalized residuals express the residual on a standard normal scale.

Let O be an observation and F the corresponding fit. The Pearson residuals are defined as: $(O-F) \Big/ st.dev.(O)$. For the multinomial distribution with sample size N:

$$st.dev.(O) = \sqrt{(1-F)F \Big/ N}.$$

For the "Coleraine" robust-normal distribution, with n observations in the sample N:

$$st.dev.(O) = \sqrt{\left((1-O)O + .01/n\right) \Big/ N}.$$

Normalized residuals are equal to the Pearson residuals for the normal error distribution and for the multinomial error distribution. For the lognormal error distribution, the normalized residual is:

$$\ln(O/F) \Big/ st.dev.(O)$$

Normalized residuals are not defined for the robust normal error distribution, which is not a proper density function. However, on the basis that the robust normal likelihood tends towards a constant as deviations approach ± 3 standard deviations from the fitted values, we calculate an approximate-normalized residual for the robust normal distribution by truncating residuals at ± 3.

Appendix Table 1. The number of parameters estimated for each model. For HCAM the number of parameters estimates is run dependent so where parameters are only estimated in some runs, this is indicated.

Parameter	*EASM-like*	*NASM-like*	*HCAM*
R_0	1	1	1
d_i^R	55	62	62
h		1	1
ψ_1	1		1
ψ_2			1 R8-R12
d_i^M		55	54 R9-R14
σ_R^2		1	1
$\gamma_{p,k}$	2		4 R1; 2 R2; 7 R3-R14
$d_{t,p}^S$		79-120	79-120 R11 & R12
v_k	2		2 R2
d_i^A	55		
η_j	5		
$F_{t,p}^*$	79-120		
q_1, q_2	1	1	2 R8 & R12, 1 otherwise
a^-, a^+			2 R5-R14
Total	201-250	200-249	Variable by run, see Table 8

Appendix Table 2. Fixed and assumed values in the EASM-like, the NASM-like, and the HCAM model runs.

Parameter	*EASM-like*	*NASM-like*	*HCAM*
σ_i	0.0707 $1951 \le i \le 2005$	0.35 $1951 \le i \le 1987$ 0.25 $1988 \le i \le 2005$	0.4 $1951 \le i \le 1987$ 0.35 $1988 \le i \le 2005$
σ_C	0.0707	N/A	N/A
σ_h	N/A	0.25	0.25
σ_{S-R}	N/A	0.2	0.2
σ_M	N/A	0.2	0.1
σ_S	N/A	0.3	0.3
σ_A	N/A	N/A	0.3
$\sigma_{\bar{M}}$	N/A	N/A	0.2
q_2	1	1	1, except R8 & R12, where estimated
$S_{process_error}$	N/A	$1/0.003$ R1-R12, R14 $1/0.009$ R13	N/A
f_p	{0.9, 0.05, 0.05} p=1,2,3	{1,0,0} p=1,2,3	{0.45, 0.45, 0.1} p=1,2,3
m_j	N/A	N/A	{0.25, 0.9, 1,1,1,1,1,1,1} j=2,3,4,…10

Appendix Table 3. Estimates of the negative log-likelihood and prior contributions to the objective function (described in the Table 5 caption) for the HCAM model runs.

		Negative log-likelihood values and contribution of priors to the objective function								
Run	*Stock*	*Total*	*Age comp.*	*Spawn data*	*Sel. Devs.*	*M devs*	*S-R resids*	*Sigma R*	*h*	*m*
R1	*GS*	1265.0	1225.0	46.7	0	0	-7.63	0.06	0.24	0.71
	WCVI	1141.3	1059.3	55.1	0	0	24.54	0.46	1.92	0.01
	CC	1482.1	1397.4	54.3	0	0	28.32	0.48	1.47	0.11
	PRD	2653.9	2579.2	41.0	0	0	31.06	0.56	1.89	0.24
	QCI	1576.5	1433.0	92.6	0	0	47.15	1.88	1.76	0.00
R2	*GS*	1173.7	1136.6	45.2	0	0	-9.64	0.09	0.41	1.06
	WCVI	1153.0	1060.8	68.9	0	0	21.02	0.36	1.92	0.08
	CC	1473.3	1371.0	74.3	0	0	25.56	0.41	1.92	0.05
	PRD	2610.1	2527.7	50.3	0	0	29.45	0.52	1.92	0.20
	QCI	1655.0	1450.1	158.7	0	0	42.51	1.70	1.92	0.04
R3	*GS*	1263.8	1224.8	45.5	0	0	-7.44	0.06	0.25	0.67
	WCVI	1089.2	1012.0	53.3	0	0	21.56	0.38	1.82	0.06
	CC	1322.9	1234.8	64.2	0	0	22.04	0.32	1.47	0.02
	PRD	2431.8	2345.2	63.3	0	0	21.54	0.35	1.39	0.00
	QCI	1502.4	1291.1	145.3	0	0	62.16	2.64	0.87	0.01
R4	*GS*	1100.1	1061.0	48.1	0	0	-10.43	0.10	0.34	0.96
	WCVI	1064.8	974.8	63.1	0	0	24.95	0.55	1.22	0.11
	CC	1234.2	1151.3	60.0	0	0	20.69	0.27	1.83	0.05
	PRD	2249.9	2070.3	155.3	0	0	22.86	0.47	0.13	0.86
	QCI	1506.6	1292.8	148.6	0	0	61.39	2.62	0.91	0.01
R5	*GS*	1085.1	1044.1	47.9	0	0	-8.45	0.07	0.37	1.12
	WCVI	1041.7	948.3	64.2	0	0	27.21	0.69	1.24	0.12
	CC	1214.8	1125.8	60.3	0	0	26.18	0.48	1.91	0.07
	PRD	2200.5	2013.8	158.5	0	0	26.38	0.68	0.14	1.00
	QCI	1484.6	1260.9	152.1	0	0	67.11	3.26	0.80	0.01
R6	*GS*	1014.8	975.4	49.2	0	0	-11.19	0.11	0.40	0.89
	WCVI	879.7	786.2	64.3	0	0	26.91	0.67	1.52	0.05
	CC	999.7	915.2	58.8	0	0	23.34	0.40	1.80	0.06
	PRD	1858.5	1704.2	129.8	0	0	23.64	0.61	0.01	0.22
	QCI	1173.1	1014.3	102.6	0	0	51.89	2.45	1.80	0.01
R7	*GS*	1073.5	1032.0	48 2	0	0	-8.24	0.06	0.38	1.09
	WCVI	1005.3	909.7	65.2	0	0	28.26	0.75	1.27	0.10
	CC	1148.2	1057.1	62.6	0	0	26.25	0.50	1.70	0.04
	PRD	2142.3	1959.4	154.5	0	0	26.75	0.72	0.11	0.84
	QCI	1410.1	1184.3	150.2	0	0	70.70	3.60	0.96	0.00
R8	*GS*	1055.7	1009.9	50.1	0	0	-6.09	0.03	0.50	1.33
	WCVI	911.9	817.1	63.9	0	0	27.91	0.83	1.92	0.12
	CC	1028.1	942.0	54.5	0	0	28.90	0.67	1.88	0.14
	PRD	1979.8	1866.0	85.4	0	0	26.32	0.72	1.42	0.00
	QCI	1314.6	1162.3	99.1	0	0	48.88	2.38	1.92	0.03
R9	*GS*	997.8	935.0	40.4	0	16.66	4.31	0.01	0.42	1.03
	WCVI	861.1	797.9	32.9	0	11.43	16.48	0.30	1.52	0.51
	CC	955.5	857.0	45.6	0	18.48	31.18	1.14	1.92	0.17
	PRD	1983.0	1873.2	52.4	0	19.33	35.53	1.65	0.01	0.85
	QCI	1148.9	1025.5	57.7	0	25.04	36.37	1.64	1.92	0.57

Run	Stock	Negative log-likelihood values and contribution of priors to the objective function								
		Total	Age comp.	Spawn data	Sel. Devs.	M devs	S-R resids	Sigma R	h	m
R10	GS	983.6	931.8	32.2	0	14.94	3.07	0.01	0.20	1.45
	WCVI	856.5	797.0	32.6	0	11.03	13.35	0.19	1.64	0.62
	CC	944.5	854.5	41.3	0	17.36	28.16	0.94	1.92	0.29
	PRD	1965.5	1865.7	44.7	0	17.66	34.73	1.60	0.00	1.11
	QCI	1141.4	1023.1	55.4	0	23.35	35.31	1.58	1.90	0.75
R11	GS	398.1	374.3	24.4	4.04	6.79	-13.63	0.16	0.66	1.33
	WCVI	400.6	327.9	27.6	4.56	9.10	28.69	1.00	1.13	0.60
	CC	578.9	479.6	42.7	16.02	8.76	28.09	0.90	1.92	0.07
	PRD	886.4	802.3	34.1	11.97	8.07	28.37	0.81	0.70	0.02
	QCI	590.6	474.7	45.5	8.46	10.89	46.24	2.66	1.72	0.21
R12	GS	388.6	370.3	19.3	3.95	6.15	-13.33	0.15	0.43	1.63
	WCVI	392.1	326.2	26.1	4.56	9.34	22.90	0.62	1.58	0.73
	CC	572.4	477.9	40.3	16.67	8.13	25.83	0.78	1.92	0.18
	PRD	862.3	781.6	32.5	11.69	8.04	26.74	0.74	0.74	0.08
	QCI	583.0	472.7	43.8	8.48	10.71	42.67	2.26	1.85	0.30
R13	GS	404.3	394.5	26.4	0	9.92	-30.39	0.62	1.81	1.36
	WCVI	389.0	342.4	26.9	0	8.53	9.11	0.10	1.38	0.55
	CC	460.9	385.7	38.1	0	13.30	21.18	0.55	1.92	0.08
	PRD	892.2	810.5	37.8	0	13.23	28.99	1.13	0.09	0.51
	QCI	606.3	504.3	52.2	0	17.02	29.40	1.13	1.68	0.43
R14	GS	-613.3	-640.6	32.7	0	9.32	-18.97	0.27	1.77	2.23
	WCVI	-338.6	-395.7	27.2	0	10.50	16.53	0.31	1.47	1.02
	CC	-368.6	-447.9	42.3	0	9.77	24.54	0.77	1.92	0.00
	PRD	-77.9	-149.1	31.5	0	7.91	30.21	1.29	0.20	0.05
	QCI	-153.1	-267.2	55.8	0	21.27	32.46	1.53	1.92	0.95